

C4607

From: Li, Ruixiang
Sent: Tuesday, April 16, 2002 4:13 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application NO: 09/758,593

Please do a standard search of SEQ ID NOs: 1 and 2 against both the commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10E18
Mail Box 10C01
306-0282

Point of Contact:
Toby Port
Technical Info. Specialist
CM1 6A04
703-308-3534

SEQ ID NO. 1 329 aa

Fragment of SEQ ID NO: 2 1158 NT

576 NT	SEQ ID NO: 2
253 NT	SEQ ID NO: 3
569 NT	SEQ ID NO: 4
330 NT	SEQ ID NO: 5
	SEQ ID NO: 6

RECEIVED
APR 16 2002
STIC

Variant
Fragment of SEQ ID NO: 2

255 NT	SEQ ID NO: 7
275 NT	8
315 NT	9
207 NT	10

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 4/17
Date Completed: 4/18
Searcher Prep/Review: 10
Clerical: _____
Online time: 10

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: eg
WWW/Internet: _____
Other (specify): _____

UNITED STATES
DEPARTMENT OF JUSTICE
FEDERAL BUREAU OF INVESTIGATION
WASHINGTON, D. C. 20535

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TITLE
JOURNAL
Direct Submission
Submitted (23-NAR-2001) Masatsugu Moriyama, Tottori University,
Department of Molecular Biology, Faculty of Medicine; Nishimachi
86, Yonago, Tottori 683-8503, Japan
(E-mail:moriyama@grape.med.tottori-u.ac.jp, Tel.:81-859-34-8040,
Fax:81-859-34-8274)

FEATURES

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BASE COUNT 279 a 321 c 383 g 186 t

ORIGIN

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Matches 1150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY	128	atggacttgcgttcgtggaggatgagaagcacacacggggtcagagtgagcgcctgcag	187
Dd	131	ATGGACTTGTGTTGCTGGAGGATGAGAACCACCGGGCTCAGAGTGCAGCCTCCAG	190
QY	188	aaggtgaaggccaagagcgtgcgaagactccctggacctgcggcgggagatcattc	247
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QY	248	gatgtggcggggtccagaacctcatcgactcggagagaaacgaagagagagaacg	307
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QY	308	gacgtctggccgctcgcgatgagcccccagagcccagagagatcaactggccctgtg	367
Dd	311	GACGCTTGCGCGCTTCGATGAGCCGCCAGAGCCCCGAGGAGACACTGGCCCTGTG	370
QY	368	gatgaggagaccttcctgaagctgcgtggaggggaaaaatgaagttcatgtgaaaagttc	427
Dd	371	GATGAGGAGACCTTCCTGAAAGTGCCTGCGGTGGAGGGAAAAATGAGGTGATTGAGAGTTC	430
QY	428	ctggctgacgggggttcagccgacactgcacacagttccgttcggacagcactgcaccca	487
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QY	488	gcttccctggaagccacatggaatactcctggagaagcttctagataatggggccactgtg	547
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QY	548	gacttcagatgcgttgactgcaacgccatgcattggcctgcgcggggccactta	607

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2002, 08:10:37 ; Search time 26.67 Seconds
(without alignments)
1804.409 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
Sequence: 1 MEDSAVQRATALIEORLAQ.....NGLEGNDSGRETPQVPQAQ 329

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL17:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1693	100.0	333	4 Q9GZV1	Q9GZV1 homo sapien
2	1484.5	87.7	328	11 Q9WV06	Q9WV06 mus musculus
3	677	40.0	319	6 Q9TU71	Q9TU71 oryctolagus
4	669.5	39.5	319	11 Q9Z1F0	Q9Z1F0 rattus norv
5	667	39.4	319	11 Q501A	Q501A mus musculus
6	666	39.3	319	11 Q9CR42	Q9CR42 mus musculus
7	658	38.9	319	4 Q153Z7	Q153Z7 homo sapien
8	505	29.8	102	4 Q9NQC9	Q9NQC9 homo sapien
9	276	16.3	1214	5 Q9VUX2	Q9VUX2 drosophila
10	249.5	14.7	1327	4 Q95271	Q95271 homo sapien
11	248.5	14.7	307	6 Q9N043	Q9N043 macaca fasc
12	247.5	14.6	543	10 Q9LQP7	Q9LQP7 arabidopsis
13	247.5	14.6	1166	4 Q9H2K2	Q9H2K2 homo sapien
14	247.5	14.6	1265	4 Q9HAS4	Q9HAS4 homo sapien
15	244	14.4	1050	4 Q9H014	Q9H014 homo sapien
16	241.5	14.3	592	12 Q9J4Z4	Q9J4Z4 fowlpox vir
17	241.5	14.3	1136	6 Q9N180	Q9N180 bos taurus
18	240.5	14.2	548	10 Q9LVG7	Q9LVG7 arabidopsis
19	239.5	14.1	1549	5 Q9V4B1	Q9V4B1 drosophila

20	238.5	14.1	1549	5	Q24241	Q24241 drosophila
21	238.5	14.1	1715	11	Q9ERD4	Q9ERD4 rattus norv
22	238.5	14.1	1763	11	Q9EQG6	Q9EQG6 rattus norv
23	237.5	14.0	247	10	Q9Z079	Q9Z079 arabidopsis
24	235	13.9	1031	4	Q9DF42	Q9DF42 homo sapien
25	234.5	13.9	1719	4	Q13768	Q13768 homo sapien
26	234.5	13.9	1856	4	Q99407	Q99407 homo sapien
27	234	13.8	1159	5	Q9NCP8	Q9NCP8 drosophila
28	234	13.8	1430	11	Q9JJF7	Q9JJF7 mus musculus
29	234	13.8	2443	5	Q9VSA2	Q9VSA2 drosophila
30	233.5	13.8	1848	11	Q61302	Q61302 mus musculus
31	231.5	13.7	843	11	Q97582	Q97582 rattus norv
32	231	13.6	271	4	Q9NPL9	Q9NPL9 homo sapien
33	231	13.6	1181	5	Q9XZ37	Q9XZ37 drosophila
34	231	13.6	1181	5	Q9VBP3	Q9VBP3 drosophila
35	230	13.6	411	11	Q9D4D8	Q9D4D8 mus musculus
36	230	13.6	1943	11	Q61307	Q61307 mus musculus
37	229	13.5	4377	4	Q12955	Q12955 homo sapien
38	228.5	13.5	318	13	Q91974	Q91974 gallus gall
39	228.5	13.5	2119	5	Q9VAU5	Q9VAU5 drosophila
40	228	13.5	637	5	Q9VUW9	Q9VUW9 drosophila
41	228	13.5	762	5	Q9VVR3	Q9VVR3 drosophila
42	228	13.5	1088	4	Q13484	Q13484 homo sapien
43	226.5	13.4	272	10	Q9AUM0	Q9AUM0 oryza sativ
44	226	13.3	627	10	Q9SYK5	Q9SYK5 arabidopsis
45	226	13.3	669	4	Q9BSK4	Q9BSK4 homo sapien

ALIGNMENTS

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AC Q9GZV1
DT 01-MAR-2001 (TREMREL. 16, Created)
DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
DE SKELETAL MUSCLE ANKYRIN PROTEIN 2 (SKELETAL MUSCLE ANKYRIN REPEAT).
GN ANKRD2
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fallavacini A., Kojic S., Bean C., Vainzof M., Salamon M.,
RA Ivoletta C., Bortolotto G., Pacchioni B., Trevisan S., Faulkner G.,
RA Lanfranchi G., Valle G.;
RT "Characterization of human skeletal muscle Ankrd2";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ304805; CAC19412.1;
DR EMBL; AJ304804; CAC19411.1;
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 5
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
SQ SEQUENCE 333 AA; 37151 MW; 679736F0491467A8 CRC64;

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Best Local Similarity 100.0%; Pred. No. 3e-109;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 5 MEDSAVQRATALIEORLAQEEENKLRGDTKQLPMDLLVLEDEKHGAQSAALQKVKG 64

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Db 65 QERVKRTSLDLRREIDVGGIQLNLIELRRKKRKRDLAALASHEPPPEETITGPVDEET 124

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Db 125 FLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFOD 184
QY 181 RLDCTAMHWACRGHLEVVKKLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFSLGL 240
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Db 245 EINARDREGDTALHDVRLNRKYIKLLHGHADMNTKLNAGKTPDVLVQLWQADTRHAL 304
QY 301 EHPEPGAENHGLEPNDSGRETPQVPAPQ 329
Db 305 EHPEPGAENHGLEPNDSGRETPQVPAPQ 333

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DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE SKELETAL MUSCLE AND CARDIAC PROTEIN (ANKYRIN REPEAT DOMAIN 2).
GN ANKRD2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DIAPHRAGM MUSCLE;
RA Ievoliella C., Formentin E., Lanfranchi G.;
RT "Characterization of a member of a new family proteins with ankyrin repeats.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TISSUE-SPLEEN, AND SKELETAL MUSCLE;
RX MEDLINE-20334618; PubMed-10873377;
RA Kemp T.J., Sadusky T.J., Saltis F., Carey N., Moss J., Yang S.Y.,
RA Sassoon D.A., Goldspink G., Coulton G.R.;
RT "Identification of Ankr2, a novel skeletal muscle gene coding for a stretch-responsive ankyrin-repeat protein.";
RL Genomics 66:229-241(2000). ID=6157400
EMBL; AJ011118; CAB46646.1; -
EMBL; AJ245346; CAB99432.1; -
EMBL; AJ245514; CAB99431.1; -
HSSP; P25963; 1IKN.
DR MGD; MGI:1861447; Ankr2.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
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Best Local Similarity 88.8%; Pred. No. 7.1e-95;
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Db 1 MEGPEAVORATLIEORLAQEEETELRRSAPGLSMDMLVLEEKRLGVQSPALQKVG 60
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Db 61 QERVKTSLDLREIIVDVGIONLIELRKKRKKOKKRDALAAASHEPPEEITGPVNEET 120
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Db 181 RLDCTAMHWACRGHLEVVKKLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFSLGL 240
QY 241 EINARDREGDTALHDVRLNRKYIKLLHGHADMNTKLNAGKTPDVLVQLWQADTRHAL 300
Db 241 DINARDREGDSALHDVRLNRKYIKLLHGHADMNTKLNAGKTPDVLVQLWQADTRHAL 300
QY 301 EHPEPGAENHGLEPNDSGRETPQVPAPQ 329
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AC QY071:
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DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CARP
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20011295; PubMed-10542334;
RA Aihara Y., Kurabayashi M., Arai M., Kedes L., Nagai R.;
RT "Molecular cloning of rabbit CARP cDNA and its regulated expression in adriamycin-cardiomyopathy.";
RL Biochim. Biophys. Acta 1447:318-324(1999).
DR EMBL; AF131883; AAF3817.1; -
DR HSSP; Q00421; 1AWC.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
SQ SEQUENCE 319 AA; 36245 MW; C7EF87A02936FED3 CRC64;

Query Match 40.0%; Score 677; DB 6; Length 319;
Best Local Similarity 46.4%; Pred. No. 3.2e-39;
Matches 136; Conservative 54; Mismatches 69; Indels 34; Gaps 3;

QY 29 GDTROKLPMDLLVLEDEKHGGAQAALOKVGOE-----RV 64
Db 18 GETGEFLP-----DDFRDQGYEAATSEKEDLKLTPAHVSVLAEOQWEREKQLEAE 70
QY 65 RKTSLDLRREIIVDVGIONLIELRKKRKKOKKRDALAAASHEPPEEITGPVDEETFLKA 124
Db 71 KKKLQSRSKLENLEDELEIIQLKRRKKYRKVPVAKL---PEPIITEPVDVPFLKA 127
QY 125 AVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFODRLDC 184
Db 128 ALENKLAIVYVEKFLSDQNNPDVDEYKRTALHRACLEGLAIVEKLMGAQAIEFRDMLRS 187
QY 185 TAMHWACRGHLEVVKKLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFSLGLEINA 244
Db 188 TAIHWACRGHLEVVKKLQSHGADTNVRDKLLSTALHVAVRTGHYECADHFACEADLNA 247
QY 245 ROREGDTALHDVRLNRKYIKLLHGHADMNTKLNAGKTPDVLVQLWQADTR 297
Db 248 KOREGDTPLHDVRLNRKYIKMIRLLINYGADLTIKNSAGKTPMDLVLNWQNGTK 300

RESULT 4
QY21F0 PRELIMINARY; PRT; 319 AA.
ID QY21F0
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QY 1096 gccagccttttctgcatgatccagagagacacataccacaaataccacataaaaaag 1155
Db 12609 GCCAGCCTTTTCTGATGATCCAGGAGCAGACATACCACAACTACCACATAAAAAAG 12668
QY 1156 ctg 1158
Db 12669 CTG 12671
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LOCUS Homo sapiens chromosome 10 clone RP11-548K23, *** SEQUENCING IN
DEFINITION PROGRESS ***, 3 unordered pieces.
ACCESSION AL355315
VERSION AL355315.12 G&L15141465
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163214)
Direct Submission
Submitted (06-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15041819.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA548K23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 162481 bases at least Q40
Consensus quality: 162660 bases at least Q30
Consensus quality: 162811 bases at least Q20
Insert size: 163014; sum-of-contigs
Quality coverage: 10.60x in Q20 bases; sum-of-contigs Quality
coverage: 10.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42225: contig of 42225 bp in length
* 42226 42325: gap of 100 bp
* 42326 139511: contig of 97186 bp in length
* 139512 139611: gap of 100 bp
* 139612 163214: contig of 23603 bp in length.
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source

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ORIGIN
Query Match 26.0%; Score 301.4; DB 2; Length 163214;
Best Local Similarity 99.7%; Pred. No. 7.2e-49;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 856' cctggaggaagaccgacgagcctgtggtgagctctgagcagctgatacccgagcgc 915
Db 12347 CCAGGCAGAAAGACCCGACGACCTGGTGCAGCTCTGGCAGGTGATACCCGCGACGC 12406
QY 916 cctggagcactcctgagccgggggctgagcataacgagcgtgaggggctaatgattg 975
Db 12407 CCTGGAGCATCTGAGCGGGGCTGAGCATAGCGGCTGAGGGGCTTAATGATGTGG 12466
QY 976 gcagagaccctcagcctgtgccagccagctgaatgctcccgagcccgagcagctac 1035
Db 12467 GCGAGAGACCCCTGAGCTGTGCCAGCCAGTGAATGCTGCCAGCCAGCCAGCTAC 12526
QY 1036 ccagccctctctgtgagccggaggtgcttaagaatgctcccgagctaaactaggg 1095
Db 12527 CCAGCCCTCTGTGTGACGCGAGGGTCTTAAGATGCTCCCGAGGTAAGTGGG 12586
QY 1096 gccagccttttctgcatgatccagagagacacataccacaaataccacataaaaaag 1155
Db 12587 GCCAGCCTTTTCTGATGATCCAGGAGCAGACATACCACAACTACCACATAAAAAAG 12646
QY 1156 ctg 1158
Db 12647 CTG 12649
RESULT 8
AL359388 218959 bp DNA HTG 02-AUG-2001
LOCUS Homo sapiens chromosome 10 clone RP11-445I23, *** SEQUENCING IN
DEFINITION PROGRESS ***, 15 unordered pieces.
ACCESSION AL359388
VERSION AL359388.21 GI:15041841
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218959)
Clark.S.
Direct Submission
Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 30, 2001 this sequence version replaced gi:15022209.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: BA445I23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: dye-terminator Big Dye; 100% of reads
Consensus quality: 162481 bases at least Q40
Consensus quality: 162660 bases at least Q30
Consensus quality: 162811 bases at least Q20
Insert size: 163014; sum-of-contigs
Quality coverage: 10.60x in Q20 bases; sum-of-contigs Quality
coverage: 10.65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 42225: contig of 42225 bp in length
* 42226 42325: gap of 100 bp
* 42326 139511: contig of 97186 bp in length
* 139512 139611: gap of 100 bp
* 139612 163214: contig of 23603 bp in length.
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/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-548K23"
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 08:09:16 ; Search time 1721.2 Seconds
(without alignments)
11099.078 Million cell updates/sec

Title: US-09-758-593A-2

Perfect score: 1158

Sequence: 1 cagctcggagcgcaccca.....ctaccacataaaaaagctg 1158

coring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Minimal number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:**

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2: gb_hgt:**

3: gb_in:**

4: gb_om:**

5: gb_ov:**

6: gb_pat:**

7: gb_ph:**

8: gb_pi:**

9: gb_pr:**

10: gb_ro:**

11: gb_sts:**

12: gb_sy:**

13: gb_un:**

14: gb_vi:**

15: em_ba:**

16: em_fun:**

17: em_hum:**

18: em_in:**

19: em_om:**

20: em_or:**

21: em_ov:**

22: em_pat:**

23: em_ph:**

24: em_pl:**

25: em_ro:**

26: em_sts:**

27: em_sy:**

28: em_un:**

29: em_vi:**

30: em_htgo_hum:**

31: em_htgo_inv:**

32: em_htgo_rod:**

33: em_htg_hum:**

34: em_htg_inv:**

35: em_htg_rod:**

36: em_htg_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149.4	99.3	1169	9	AB058599 Homo sapi
2	1109.8	95.8	1159	9	AJ304805 Homo sapi
3	761	65.7	1100	10	AJ011118 Mus muscu
4	759.4	65.6	1100	10	AJ245514 Mus muscu
5	302	26.1	307	9	AJ249975 Homo sapi
6	301.4	26.0	14300	9	AJ304804 Homo sapi
7	301.4	26.0	163214	2	AL355315 Homo sapi
8	301.4	26.0	218959	2	AL359388 Homo sapi
9	264.8	22.9	1758	6	AX140502 Sequence
10	261.6	22.6	1026	10	AF041847 Mus muscu
11	256.8	22.2	1749	10	U50736 Rattus norv
12	248.4	21.5	1901	9	X83703 H. sapiens m
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14	243.6	21.0	1940	4	AF131883 Oryctolag
15	131.8	11.4	9876	10	AJ249346 Mus muscu
16	113.4	9.8	386	6	AX071347 Sequence
17	103.8	9.0	363	6	AX071332 Sequence
18	91.6	7.9	222	10	AF041849 Mus muscu
19	88.2	7.6	6192	9	M28880 Human eryth
20	87.2	7.5	5080	9	AB023174 Homo sapi
21	86.6	7.5	7252	9	X16609 Human mRNA
22	86.6	7.5	197748	2	AC026283 Homo sapi
23	85.8	7.4	6278	9	X56958 Homo sapien
24	85.8	7.4	12518	9	Z26634 Homo sapien
25	85	7.3	67923	9	AL391244 Human DNA
26	84.6	7.3	2754	9	AB028932 Homo sapi
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28	84.6	7.3	17173	9	AB058779 Homo sapi
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40	77.6	6.7	1742	9	AB046089 Macaca fa
41	77.4	6.7	1934	5	AF296130 Gallus ga
42	77.2	6.7	1135	9	AF105427 Homo sapi
43	77.2	6.7	1288	6	AR088277 Sequence
44	77.2	6.7	1345	6	AX025001 Sequence
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ALIGNMENTS

RESULT 1

AB058599

LOCUS

DEFINITION

AB058599

AB058599

AB058599.1

GI:14495177

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

AB058599 1169 bp mRNA 27-JUN-2001
Homo sapiens arpp mRNA for ankyrin-repeat protein, complete cds.

AB058599
Homo sapiens arpp mRNA for ankyrin-repeat protein, complete cds.

AB058599.1 GI:14495177
Homo sapiens esophageal carcinoma cell_line:TEL cdna to mRNA.

Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (sites)
Moriyama,M., Tsukamoto,Y., Fujiwara,M., Kondo,G., Nakada,C.,
Baba,T., Ishiguro,N., Miyazaki,A., Nakamura,K., Hori,N., Sato,K.,
Shomori,K., Takeuchi,K., Sato,H., Mori,S. and Ito,H.

Identification of a novel human ankyrin-repeated protein homologous
to CARP

Biochem. Biophys. Res. Commun. (2001) In press

2 (bases 1 to 1169)
Moriyama,M.

Thu Apr 18 10:26:05 2002

TITLE Direct Submission
JOURNAL Submitted (23-MAR-2001) Masatsugu Moriyama, Tottori University,
Department of Molecular Biology, Faculty of Medicine, Nishimachi
86, Yonago, Tottori 683-8503, Japan
(E-mail: moriyama@grape.med.tottori-u.ac.jp, Tel: 81-859-34-8040,
Fax: 81-859-34-8274)

FEATURES
Location/Qualifiers
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QY 908 cggcagcctctgagcattcctgagccgggggtgagcagcagcagcagcagcagcagcagc 967
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QY 1148 taaaaagctg 1158
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RESULT 2
HSA304805 1159 bp mRNA PRI 21-DEC-2000
LOCUS Homo sapiens mRNA for skeletal muscle ankyrin protein 2 (ANKRD2
DEFINITION gene)
ACCESSION AJ304805 GI:11967782
VERSION AJ304805.1
KEYWORDS ANKRD2 gene; skeletal muscle ankyrin protein 2.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1159)
AUTHORS Pallavicini A., Kojic S., Bean C., Vainzof M., Salamon M.,
Ievolella C., Bortoletto G., Pacchioni B., Trevisan S.,
Faulkner G., Lanfranchi G. and Valle G.
TITLE Characterization of human skeletal muscle Ankrd2
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1159)
AUTHORS Pallavicini A.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-2000) Pallavicini A., Biologia, Università di
Padova, via Ugo Bassi 58/b, 35100, ITALY
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DEFINITION Mus musculus mRNA for a skeletal muscle and cardiac protein.
ACCESSION AJ011118
VERSION AJ011118.1 GI:5420271
KEYWORDS skeletal muscle and cardiac protein.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 1100)
AUTHORS Kemp,T.J., Sadusky,T.J., Saltisi,F., Carey,N., Moss,J., Yang,S.Y.,
Sassoon,D.A., Goldspink,G. and Coulton,G.R.
TITLE Identification of Ankr2, a novel skeletal muscle gene coding for a
stretch-responsive ankyrin-repeat protein
JOURNAL Genomics 66 (3), 229-241 (2000)
MEDLINE 20334618
REFERENCE 2 (bases 1 to 1100)
AUTHORS Ievolella,C., Formentin,E. and Lanfranchi,G.
TITLE Characterization of a member of a new family proteins with ankyrin
repeats
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1100)
AUTHORS Ievolella,C.
TITLE Direct Submission
JOURNAL Submitted (30-SEP-1998) Ievolella C., CRIBI Biotechnology Centre,
Universita di Padova, via G. Colombo 3 Padova, 35121, ITALIA
COMMENT Related sequence F18281.
FEATURES Location/Qualifiers
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Qy 550 ctccagagatcggtgagctgcacagccatgcattggcctgcgcgcgcgcgcgcgcgcgcgc 609
Db 541 CTCCTCAGGATCGCTGGAGCTGCACAGCCATGCACCTGGCCCTGCCGTGGGGCCACCTGA 600
Qy 610 ggtggtgaaactctgaaacatggagcagacacccaatgtgagggataagcctcag 669
Db 601 GGTGTGAGACTCTCTGAAAGCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 660
Qy 670 caccgcgctgcagctggcagtcgcgacagggcaggtggagagtgtggagcactttctatc 729
Db 661 CACTCCCTGCATGTGGCGTCCGTACTGGACACCTGGAGATTGTGGAACATTTCTTTC 720
Qy 730 cctgggctggaatcaatgcagagagaggggaggggaggggaggggaggggaggggagggg 789
Db 721 CCTGGCTTGGATATCAATGCCAAAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Qy 790 gaggctcaacgcgtcaaaaatcaataactcaactgctgctcgtcgtgaggggaggggagggg 849
Db 781 GAGACTCAACCGCTCAAAAATCATCAAACTGCTGCTTGTGATGGGGGGGAGCATGATGCG 840

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Qy 850 caaqaacctggcagaaagaccacgagcactggtgagctgagctgagcaggtgataccgc 909
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Qy 910 gcagccctgagcatcctgagcgggggctgagcacaacgggctggaggggcctaatga 969
Db 901 GCATGCCCTGGAGCATCCCGAGCCAGAATCAGAGCAGAACGAGCTGGAGAGGCC---TGG 957
Qy 970 tagtggggagagaccctcagcctgtgcccagccagtcgaatgctgcccagccagccagc 1029
Db 958 GAGTGGCGTGAGACACCTCAGCCTTATACCGCCAGTAAATACCTACCCGAGGTGGGC 1017
Qy 1030 agctaccagccctctctgtgctgagcggggtcctaaagaatggtcccccggagctaa 1089
Db 1018 ACCCAACCCCTACTATGAGCTGCTGCAGCCAGCTCTAGCAGGAACACCCCTAGATGCA 1077
Qy 1090 c 1090
Db 1078 c 1078

RESULT 5
HSA249975 307 bp mRNA PRI 25-JUL-2000
LOCUS Homo sapiens partial mRNA for ankyrin repeat domain 2 (stretch responsive muscle).
ACCESSION AJ249975
VERSION AJ249975.1 GI:9501289
KEYWORDS Ankr2 gene; ankyrin repeat domain 2; stretch responsive muscle.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 307)
AUTHORS Kemp,T.J., Sadusky,T.J., Saltisi,F., Carey,N., Moss,J., Yang,S.Y., Sassoon,D.A., Goldspink,G. and Coulton,G.R.
TITLE Identification of ankr2, a novel skeletal muscle gene coding for a stretch-responsive ankyrin-repeat protein
JOURNAL Genomics 66 (3), 229-241 (2000)
MEDLINE 20334618
REFERENCE 2 (bases 1 to 307)
AUTHORS Kemp,T.J.
TITLE Direct Submission
JOURNAL Submitted (13-OCT-1999) Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, 6F Building Level 2, Exhibition Road, South Kensington, London, UNITED KINGDOM
COMMENT Related sequence: AJ245514.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/tissue_type="skeletal muscle"
1..307
/gene="ANKRD2"
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/db_xref="GI:9501290"
/translation="SAQEEENEKLGRDXRKLPMDDLVLLEDEKHHGAQSAALQKVKGO ERVRKTSLDLRREIIVDGGIQLNLTRELKRRKKRDALAAASHEPPEETITGPVDEE"
BASE COUNT 76 a 82 c 110 g 38 t 1 others
ORIGIN
Query Match 26.1%; Score 302; DB 9; Length 307;
Best Local Similarity 99.7%; Pred. No. 2.5e-48;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	5	GCACAGGAGGAGGAATGAGAAATCCGAGGAGACNACGCCAGAACTGCCCATGGAC	64
QY	134	ttctagtctgagatgagagcaccacggggtccagagtgcagccctcgagaagtg	193
Db	65	TTGCTGTGTGGAGATGAGAGCACCACGGGCTCAGAGTGCAGCCCTCGAGAAGGTG	124
QY	194	aagggccaagcgctgcgcaagcgtccctggacctgcggcgaggagatcatcatgtg	253
Db	125	AAGGCCAACAGCGCTGCGCAAGAGCTCCCTGGACCTCGCGGGGAGATCATCATGTG	184
QY	254	ggcggatccagaacctcatcgactcggaagaacgcaagcagaagcggagcgcgt	313
Db	185	GGCGGGATCCAGAACCTTCATCGAGCTGCGGAGAAACGCAAGCAGAGAAGCGGACGCT	244
QY	314	ctgcccctctgcatgagccgccccagagcccgagagcagatcactggccctgtgatatgag	373
Db	245	CTGCGCGCTCGCATGAGCGCCCGCAGAGCCGAGATCATCTGCCCTGTGGATGAG	304
QY	374	gag 376	
Db	305	GAG 307	
RESULT 6			
HSA304804			
LOCUS			
DEFINITION Homo sapiens ANKRD2 gene for skeletal muscle ankyrin repeat, exons 1-9.			
ACCESSION AJ304804			
VERSION AJ304804.1 GI:11967780			
KEYWORDS ANKRD2 gene; skeletal muscle ankyrin repeat.			
SOURCE human.			
ORGANISM Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1 (bases 1 to 14300)			
AUTHORS Pallavicini, A., Kojic, S., Bean, C., Vainzof, M., Salamon, M., Ievolella, C., Bortolotto, G., Pacchioni, B., Trevisan, S., Faulkner, G., Lanfranchi, G. and Valle, G.			
TITLE Characterization of human skeletal muscle Ankrd2			
JOURNAL Unpublished			
REFERENCE 2 (bases 1 to 14300)			
AUTHORS Pallavicini, A.			
TITLE Direct Submission			
JOURNAL Submitted (18-DEC-2000) Pallavicini A., Biologia, Universita di Padova, via Ugo Bassi 58/b, 35100, ITALY			
FEATURES			
source			
1. 14300			
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916 cctgagcatcctgagccggggtgagcacaacggtgaggggcccataatgatgtgg 975			
12429 CTTGAGGATCTTGGCGGGGCTGAGCATACGGGCTGGAGGGGCTAATGATAGTG 12488			
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QY			

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Db 12489 GCGAGAGACCCCTCAGCCGTGTGCCAGCCAGTGAATGCGTCCCGCAGCCAGCCAGCTAC 12548
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Qy 1036 ccagccctctgtgtcacccgaggtctctaagaatgctccggagctaactgagg 1095
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Db 12549 CCAGCCCTCTCTGTGTGTCAGCCGAGGGTCTTAAGATGCTCCCGAGCTAACTGAGG 12608
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Qy 1096 gccagccttttttgcagcagcagcacataccacacaaataacacataaaaaag 1155
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Db 12669 CTG 12671
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RESULT 7
AL355315 163214 bp DNA HTG 07-AUG-2001
LOCUS Homo sapiens chromosome 10 clone RP11-548K23, *** SEQUENCING IN
DEFINITION PROGRESS ***, 3 unordered pieces.
ACCESSION AL355315
VERSION AL355315.12 GI:15141465
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 163214)
Chapman, J.
Direct Submission
Submitted (06-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Aug 9, 2001 this sequence version replaced gi:15041819.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba548K23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 162483 bases at least Q40
Consensus quality: 162860 bases at least Q20
Consensus quality: 162811 bases at least Q20
Insert size: 163014; sum-of-contigs
Quality coverage: 10,60x in Q20 bases; sum-of-contigs Quality
coverage: 10,65x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* as soon as it is available and the accession number will
* be preserved.
* 1 42225: contig of 42225 bp in length
* 42226 42325: gap of 100 bp
* 42326 139511: contig of 97186 bp in length
* 139512 139611: gap of 100 bp
* 139612 163214: contig of 23603 bp in length.
Location/Qualifiers
1. 163214
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="10"
/clone="RP11-548K23"
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FEATURES
source
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ORIGIN
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Query Match 26.0%; Score 301.4; DB 2; Length 163214;
Best Local Similarity 99.7%; Pred. No. 7.2e-49;
Matches 302; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 856 cctggcagaagaccccgacgacctggtgcagctctggcagctgatacccgcaagc 915
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Db 12347 CCAGCAGGAAAGACCCCGACGACCTGGTGCAGCTCTGGCAGGCTGATACCCGCGCAGC 12406
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Qy 916 cctggagacatcctgagccgggggtgagcataacgggctggaggccctaagtgg 975
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Qy 976 gcgagagaccctcagcctgtgccagccagtgatgcgtgccccagcccgagctac 1035
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Qy 1036 ccagccctctctgtgtgcagccggggtctctaagaatgctcccgagctaaatgagg 1095
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Db 12527 CCAGCCCTCTCTGTGTGTCAGCCGAGGGTCTTAAGAATGGTCTCCGGAGCTAACTGAGG 12586
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Qy 1096 gccagccttttttgcagcagcagcacataccacacaaataacacataaaaaag 1155
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Db 12587 GCCAGCCCTTTTCTGTCATGATCCAGGAGCAGATACCACAAATACCACATAAAAAAG 12646
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Qy 1156 ctg 1158
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Db 12647 CTG 12649
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RESULT 8
AL359388 218959 bp DNA HTG 02-AUG-2001
LOCUS Homo sapiens chromosome 10 clone RP11-445I23, *** SEQUENCING IN
DEFINITION PROGRESS ***, 15 unordered pieces.
ACCESSION AL359388
VERSION AL359388.21 GI:15041841
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 218959)
Clark, S.
Direct Submission
Submitted (01-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 30, 2001 this sequence version replaced gi:15022209.
----- Genome Center
Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: ba445I23
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
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RESULT	9
AX140502	DNA
LOCUS	1758 bp
SEQUENCE	Sequence 124 from Patent EP1114862.
DEFINITION	AX140502
ACCESSION	AX140502.1 GI:14280621
VERSION	
KEYWORDS	house mouse.
SOURCE	Mus musculus
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
REFERENCE	Wolfe, J.P., Regenberg, J. and Goppelt, A. 1 (bases 1..1758)
AUTHORS	Use of polynucleotides or their encoding nucleic acids for the diagnosis or treatment of skin diseases and their use in identifying pharmacologically active substances
TITLE	Patent: EP 1014862-A 124 11-JUL-2001;
JOURNAL	Switch Biotech Aktiengesellschaft (DE)
FEATURES	Location/Qualifiers
	1..1758

Bd 858 GATGATCGGGCTTGTATTACACTTCGGTGCGGAACCCTCAATGTACAAGAACTGTCTGGGAA 917

Gy 868 gaccgccagcactgtgctgcaggctcgccagtctgatatacc 907
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Bd 918 GATCCCTATGGATCCTGGTGTTGCCTACTGCCAANTGGAACC 957

RESULT 12

HSRNACINP HSRNACINP 1901 bp mRNA PRI 05-SEP-1995
LOCUS H.sapiens mRNA for cytokine inducible nuclear protein.
DEFINITION X83703
ACCESSION x83703.1 GI:793840
VERSION ankryn-like repeat; nuclear localisation signal; nuclear protein.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1901)
AUTHORS Chu,W., Burns,D.K., Swerlick,R.A. and Presky,D.H.
TITLE Identification and characterization of a novel cytokine-inducible
J. Biol. Chem. 270 (17), 10236-10245 (1995) nuclear protein; from human endothelial cells
MEDLINE 95247734
AUTHORS J. Biol. Chem. 270 (17), 10236-10245 (1995)

FEATURES source
Direct Submission
Submitted (05-JAN-1995) W. Chu, Hoffmann-La Roche, 340 Kingsland
Street, Dept. of Inflammation/Autoimmune Disease, Hoffmann-La
Roche, Nutley, NJ 07110, USA
Location/Oualifiers
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organism="Homo sapiens"
db_xref="taxon:9606"
chromosome="10"
tissue_type="skin"
cell_type="endothelial"
clone_lib="HDMEC CDNA"
clone="C-193"
1..1901 misc_feature 94..98 /note="nuclear localization signal"
repeat_unit 152..283 /note="ankyrin-like repeats"
CDS 250..1209 /note="cytokine-inducible expression"

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 Qy 518 gagaagctctagataaattggggccactgtgacttccaggatcggtgactgcacagcc 577
 Db 757 GAGAAAGTTAATGGAAAGCTGGAGCCAGATCGAAATTCCTGTATGCTTGAATCCACAGCC 816
 Qy 578 atgcattggctgcgcggggccacttagaggtggtgaaactctctgaaagccatgga 637
 Db 817 ATCCACTGGGCAAGCCGTGGAGGAACCTGGATGTTTTAAATTTGTTGCTGAATAAGA 876
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 Db 877 GCAAAATTAAGCCCGAGATAAGTTGCTACGACAGCGCTGCATGTGCGGTGAGGACT 936
 Qy 698 gggcaggtggagattgtgagcaacttctatccctggcgcgtggaatacaatgcacagac 757
 Db 937 GGCCTATGAGTGGCGGAGCATCTTATCGCCTGTGAGGCAGACCTCAACGCCAAAGAC 996
 Qy 758 agggaggggactgctccctcatgacgtgtgagcctcaaccgcctacacaaatcatcaa 817
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 Qy 818 ctgctgctctgcattggtggctgacatgatgacacgaacacctggcaggaaagaccccgag 877
 Db 1057 CTCTCTGATTATGATGCGCGGATCTCAACATCAAGAACTGTGCTGGGAAGACGCGGATG 1116
 Qy 878 gacctgggtgagctctgagcagctgatacc 907
 Db 1117 GATCTGGTCTACACTGGCAGAGTGAAC 1146

RESULT 13
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 LOCUS human STS SHGC-35401, sequence tagged site.
 DEFINITION G28603
 ACCESSION G28603
 VERSION G28603.1 GI:1408418
 KEYWORDS STS; STS sequence; primer; sequence tagged site.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1901)
 Myers, R. M.
 Unpublished (1996)

Contact: Richard M. Myers
 Stanford Human Genome Center (SHGC)
 Stanford University School of Medicine
 Department of Genetics, M-344, Stanford, CA 94305, USA
 Tel: 4157259687
 Fax: 4157259689
 Email: myers@shgc.stanford.edu

Primer A: GGCATTTTGAAGGCATGG
 Primer B: CCAGATGGATCATCAAGG
 STS size: 222
 PCR Profile:

Initial incubation: 94 degrees C for 90 seconds
 Denaturation: 94 degrees C for 15 seconds
 Annealing: 62 degrees C for 23 seconds
 Polymerization: 72 degrees C for 30 seconds
 PCR Cycles: 30
 Thermal Cycler: Perkin Elmer 9600

Protocol:
 Template: 25 ng
 Primer: each 1 uM
 dNTPs: each 200 uM
 Taq Polymerase: 0.05 units/uL
 Total Vol: 10 uL

Buffer: MgCl2: 2.5 mM
 KCl: 50 mM
 Tris-HCl: 20 mM
 pH: 8.3
 Prepared with primer pairs provided by Sandoz, derived from X83703
 -- Washington University/Merck EST sequence.
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 /db_xref="taxon:9606"
 /map="10"
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 primer_bind complement(1447..1467)
 BASE COUNT 592 a 378 c 460 g 471 t
 ORIGIN

Query Match 21.5%; Score 248.4; DB 11; Length 1901;
 Best Local Similarity 64.7%; Pred. No. 3.3e-38;
 Matches 369; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
 Qy 338 ccagagcccgagagatcactgcccctgtggatgagagacaccttctctgaaagctgcggtg 397
 Db 577 CCAGAACCTGAAATCATATACGGAACCTGTGGATGTGCCTACGTCTTCTGAAGGCTGCTCTG 636
 Qy 398 gaggggaaaaatgaagtcattgagaagttccttgcgtgacggggggtgcacacagctgc 457
 Db 637 GAGAATAAATGCCAGTAGTAGAAAAATTTCTGTGACAGCAAGAACAATCCAGATGTTTGT 696
 Qy 458 gaccagttccgtcgacagcactgcacagacgttccctggaggccacatgaaatcctg 517
 Db 697 GATGAGTATAAAGCGACAGCTCTTCATAGAGCATGCTTGGAAAGGACATTTGGCAATTGTG 756
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 Qy 578 atgcattggctgcgcggggccacttagaggtggtgaaactctctgaaagccatgga 637
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 Qy 698 gggcaggtggagattgtgagcacttcttctatccctgggcctggaatcaatccagagac 757
 Db 937 GGCCTATGAGTGGCGGAGCATCTTATCGCCTGTGAGGCAGACCTCAACGCCAAAGAC 996
 Qy 758 aggggaggggatactgcccctgcagctgacgtgtgaggtcaccacccgtacacacatcaaaa 817
 Db 997 AGAGAGGAGATACCCCGTTCATGATGCGGTGAGACTGAACCGTATTAAGATGATCCCA 1056
 Qy 818 ctgctgctctgcagtgaggctgacatgatgacacgaacacctggcaggaaagaccccgag 877
 Db 1057 CTCTCTGATTATGATGCGCGGATCTCAACATCAAGAACTGTGCTGGGAAGACGCGGATG 1116
 Qy 878 gacctgggtgagctctgagcagctgatacc 907
 Db 1117 GATCTGGTCTACACTGGCAGAGTGAAC 1146

RESULT 14
 AF131883
 LOCUS AF131883 1940 bp mRNA MAM 30-NOV-1999
 DEFINITION Oryctolagus cuniculus CARP mRNA, complete cds.
 ACCESSION AF131883
 VERSION AF131883.1 GI:6478316
 KEYWORDS

SOURCE	rabbit.	Db	1026	CTCCGTGATTATCTACGGTCCGACCTCAAGAACAGCGCGGAGACCCCAATG	1085
ORGANISM	Oryctolagus cuniculus	QY	878	gacctgtgtcagctctgtgcagcgtgtatacc	907
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.	Db	1086	GATCTGCTGCTAACTGCGCAAAATGAACC	1115
AUTHORS	Aihara, Y., Kurabayashi, M., Arai, M., Kedes, L. and Nagai, R.	RESULT	15		
TITLE	Molecular cloning of rabbit CARP cDNA and its regulated expression in adriamycin-cardiomyopathy	MMU249346	9876 bp	DNA	25-JUL-2000
JOURNAL	Biochim. Biophys. Acta 1447 (2-3), 318-324 (1999)	LOCUS			
MEDLINE	20011295	DEFINITION			
REFERENCE	10542334	MMU249346			
AUTHORS	2 (bases 1 to 1940)	ACCESSION			
TITLE	Direct Submission	AJ249346			
JOURNAL	Submitted (26-FEB-1999) Second Department of Internal Medicine, Gunma University School of Medicine, 3-39-15 Showa-machi, Maebashi 371-8511, Japan	VERSION	AJ249346.1	GI:9501361	
FEATURES		KEYWORDS	Ankrd2 gene; ankryrin repeat domain 2; stretch responsive muscle.		
source	1. .1940	SOURCE	house mouse.		
	/organism="Oryctolagus cuniculus"	ORGANISM	Mus musculus		
CDS	/db_xref="taxon:9986"	REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
	219. .1178	AUTHORS	1 (bases 1 to 9876)		
	/codon_start=1	TITLE	Kemp, T.J., Sadusky, T.J., Saltisi, F., Carey, N., Moss, J., Yang, S.Y., Sassoon, D.A., Goldspink, G. and Coulton, G.R.		
	/product="CARP"	JOURNAL	Identification of ankrd2, a novel skeletal muscle gene coding for a stretch-responsive ankryrin-repeat protein		
	/protein_id="AF13817.1"	MEDLINE	Genomics 66 (3), 229-241 (2000)		
	/db_xref="GI:6478317"	REFERENCE	20334618		
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	KYVPAKEPEITIEPVDVPRFLKAALENKLAIVEKFLSDQNNPDVDCYKRTALHRA	TITLE	Submitted (09-SEP-1999), Kemp T.J., Molecular Pathology, Imperial College School Of Medicine, SAF Building, Exhibition Road, South Kensington, London SW7 2AZ, UNITED KINGDOM		
	CLEGHIAIVEKLEMEAGAOIEFRDLESTAIHWACRGNLEVIKLLNKGAKISARDKL	JOURNAL	Location/Qualifiers		
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			573. .578		
		exon	/gene="Ankrd2"		
			/note="TATA signal is muscle specific"		
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			/gene="Ankrd2"		
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			QBPPEPEITGPVNEETFLKAAVEGKMKVLDKYLADGGSADTCDPEPTALHRSLE		
			GHMEILEKLENGATVDFDRDCTAHMWACRGGHLEVRLLQSGDADTNVDRKLLST		
			PLHVAVRTGHVEITVEHFLSLGIDINAKDRGDSALHDVRLNRYKILKLLHGHADMM		
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			/rpt_unit=1020. .1021		

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9484. .9733
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Best Local Similarity 62.7%; Pred. NO. 5.8e-16;
Matches 240; Conservative 0; Mismatches 137; Indels 6; Gaps 2;

QY 195 agggcgaagcgcgtgcgaagcgtccctggaccctgcgcgggagatcatcgatgtgg 254
Db 4710 AGGGCCAGAGGCGGTGCCAGAGATCCCTGGACCTGCGACGTGAGATCATTTGATGG 4769

QY 255 gcggatccagaacctcatcgactgcggaagaacgcaagcagaagaagcggagcgtc 314
Db 4770 GTGGGATCCAGAACCTCATTTGAAC TGAGGAAAAAGCAAGCAGAAAAAGCGAGATGCC 4829

QY 315 tggccgctcgcgatgagcgcgccccagagcccgagagatcactgcccctgtggatgagg 374
Db 4830 TGGCTGCAGCCAGGAGCGCTCCAGAGCCAGAGGAGATC-GTAAGGCTCCTGATTTAG 4888

QY 375 agaccttcctgaagctgcgtggagggaataaaggtcattgagaagttcctggctg 434
Db 4889 ACAGATGTGGGAGGGGGAGCGCTGGGAGGCCCGCGAAGCTCCCTTTATTTATTGGCGG 4948

QY 435 acgggggggtcagccgacacgtgcgaccagttccgtcggacagcactgcaccgagctccc 494
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Db 4949 ATGTTCTACCTGCAGAC-----CGGCCCTGTGAATGAGGAGACATTCTCTGAAAGCTGCAG 5003
QY 495 tggaaagccacatgaaatcctcctgagaagcttctagataaatgggccaactgtgaactccc 554
Db 5004 TGGAGGGGAAAAATGAAAGTCATTGACAAAGTACCTGGCGGACGGAGGTTTCAGCGGACACCT 5063
QY 555 aggatcggctggactgcacagcc 577
Db 5064 GTGATGAGGTGATCCCCCGCGGCC 5086
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Search completed: April 17, 2002, 10:07:55
Job time: 7119 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 17, 2002, 08:10:37 ; Search time 26.67 Seconds
(without alignments)
1804.409 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
Sequence: 1 MEDSEAVORATLIEQRLAQ.....NLEGPNDSGRETPOVPQA 329

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 14627329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL17.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1693	100.0	333	4 Q9GZV1	Q9gzv1 homo sapien
2	1484.5	87.7	328	11 Q9WV06	Q9wv06 mus musculus
3	677	40.0	319	6 Q9TU71	Q9tu71 oryctolagus
4	669.5	39.5	319	11 Q921F0	Q921f0 rattus norv
5	667	39.4	319	11 Q55014	Q55014 mus musculus
6	666	39.3	319	11 Q9CR42	Q9cr42 mus musculus
7	658	38.9	319	4 Q15327	Q15327 homo sapien
8	505	29.8	102	4 Q9NQC9	Q9nqc9 homo sapien
9	276	16.3	1214	5 Q9VUX2	Q9vux2 drosophila
10	249.5	14.7	1327	4 Q95271	Q95271 homo sapien
11	248.5	14.7	307	6 Q9N043	Q9n043 macaca fasc.
12	247.5	14.6	543	10 Q9LQP7	Q9lqp7 arabidopsis
13	247.5	14.6	1166	4 Q9H2K2	Q9h2k2 homo sapien
14	247.5	14.6	1265	4 Q9HAS4	Q9has4 homo sapien
15	244	14.4	1050	4 Q9H014	Q9h014 homo sapien
16	241.5	14.3	592	12 Q9J4Z4	Q9j4z4 fowlpox vir
17	241.5	14.3	1136	6 Q9N180	Q9n180 bos taurus
18	240.5	14.2	548	10 Q9LVG7	Q9lvvg7 arabidopsis
19	239.5	14.1	1549	5 Q9V4B1	Q9v4b1 drosophila

20	238.5	14.1	1549	5	Q24241	Q24241 drosophila
21	238.5	14.1	1715	11	Q9ERD4	Q9erd4 rattus norv
22	238.5	14.1	1763	11	Q9EQG6	Q9eqg6 rattus norv
23	237.5	14.0	247	10	Q9ZQ79	Q9zq79 arabidopsis
24	235	13.9	1031	4	Q9UF42	Q9uf42 homo sapien
25	234.5	13.9	1719	4	Q13768	Q13768 homo sapien
26	234.5	13.9	1856	4	Q99407	Q99407 homo sapien
27	234.5	13.8	1159	5	Q9NCP8	Q9ncp8 drosophila
28	234	13.8	1430	11	Q9JJP7	Q9jjp7 mus musculus
29	234	13.8	2443	5	Q9VSA2	Q9vsa2 drosophila
30	233.5	13.8	1848	11	Q61302	Q61302 mus musculus
31	231.5	13.7	843	11	P97582	P97582 rattus norv
32	231	13.6	271	4	Q9NPL9	Q9npl9 homo sapien
33	231	13.6	1181	5	Q9XZ37	Q9xz37 drosophila
34	231	13.6	1181	5	Q9VBP3	Q9vbp3 drosophila
35	230	13.6	411	11	Q9D4D8	Q9d4d8 mus musculus
36	230	13.6	1943	11	Q61307	Q61307 mus musculus
37	229	13.5	4377	4	Q12955	Q12955 homo sapien
38	228.5	13.5	318	13	Q91974	Q91974 gallus gall
39	228.5	13.5	2119	5	Q9VAU5	Q9vau5 drosophila
40	228	13.5	637	5	Q9VUW9	Q9vuww9 drosophila
41	228	13.5	762	5	Q9VVR3	Q9vvvr3 drosophila
42	228	13.5	1088	4	Q13484	Q13484 homo sapien
43	226.5	13.4	272	10	Q9AUW0	Q9auw0 oryza sativ
44	226	13.3	627	10	Q9SYK5	Q9syk5 arabidopsis
45	226	13.3	669	4	Q9BSK4	Q9bsk4 homo sapien

ALIGNMENTS

RESULT 1

Q9GZV1 ID Q9GZV1 PRELIMINARY; PRT; 333 AA.

AC Q9C.V1;

DT 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)

DE SKELETAL MUSCLE ANKYRIN PROTEIN 2 (SKELETAL MUSCLE ANKYRIN REPEAT).

GN ANKRD2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA Pallavicini A., Kojic S., Bean C., Vainzof M., Salamon M.,

RA Ivoletta C., Bortoletto G., Pacchioni B., Trevisan S., Faulkner G.,

RA Lanfranchi G., Valle G.;

RL "Characterization of human skeletal muscle Ankrd2.";

RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ304805; CAC19412.1;

DR EMBL; AJ304804; CAC19411.1;

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 4.

DR PRINTS; PR01415; ANKYRIN.

DR SMART; SM00248; ANK; 5.

DR PROSITE; PS50088; ANK_REPEAT; 4.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

SQ SEQUENCE 333 AA; 37151 MW; 679736F0491467A8 CRC64;

Query Match 100.0%; Score 1693; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 3e-109;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEDSEAVORATLIEQRLAQEEENEKLRGTQKLPMDLLVLEDEKHHGSAALQKVKG	60
Db	5	MEDSEAVORATLIEQRLAQEEENEKLRGTQKLPMDLLVLEDEKHHGSAALQKVKG	64
Qy	61	QERVKTSLDLRREIIVGGIQLIELKRRKKRQKRALAASHEPPEITGPVDEET	120
Db	65	QERVKTSLDLRREIIVGGIQLIELKRRKKRQKRALAASHEPPEITGPVDEET	124

Thu Apr 18 10:26:04 2002

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121 FLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
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181 RLDCATAMHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGL 240
185 RLDCATAMHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGL 244
241 EINARDREGDTALHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTRHAL 300
245 EINARDREGDTALHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTRHAL 304
301 EHPEPGAHEHNGLEPNDSGRETPQVPAQ 329
305 EHPEPGAHEHNGLEPNDSGRETPQVPAQ 333

RESULT 2
Q9WV06 PRELIMINARY; PRT; 328 AA.
AC Q9WV06;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
OC SKELETAL MUSCLE AND CARDIAC PROTEIN (ANKYRIN REPEAT DOMAIN 2).
OC ANKRD2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-DIAPHRAGM MUSCLE;
RA Revellia C., Formentin E., Lanfranchi G.;
RT "Characterization of a member of a new family proteins with ankyrin repeats."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS; TISSUE-SPLEEN, AND SKELETAL MUSCLE;
RX MEDLINE-20334618; PubMed-10873377;
RA Kemp T.J., Sadusky T.J., Saltis F., Carey N., Moss J., Yang S.Y.,
RA Sassoon D.A., Goldspink G., Coulton G.R.;
RT "Identification of Ankr2, a novel skeletal muscle gene coding for a stretch-responsive ankyrin-repeat protein."
RL Genomics 66:229-241(2000).
DR EMBL; AJ011118; CAB46646.1; -
DR EMBL; AJ249346; CAB99432.1; -
DR EMBL; AJ245514; CAB99431.1; -
DR HSP; P25963; IKN.
DR MGD; MGI:1861447; Ankrd2.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SEQUENCE 328 AA; 36707 MW; DB90D955EE9D175E CRC64;

Query Match 87.7%; Score 1484.5; DB 11; Length 328;
Best Local Similarity 88.8%; Pred. No. 7.1e-95;
Matches 292; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

QY 1 MEDSAVORATALIEORLAQEEENEKLGDRFQKLPMDLVLEDEKHHGAQSAALQKVGK 60
DB 1 MEGPEAVORATELIEORLAQEEENEKLGDRFQKLPMDLVLEDEKHHGAQSAALQKVGK 60
QY 61 QERVKRTSLDLRREIDYGGIONLIELKKRQKRDALAAASHPEEITGPVDEET 120
DB 61 QERVKRTSLDLRREIDYGGIONLIELKKRQKRDALAAASHPEEITGPVDEET 120
QY 121 FLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180

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121 FLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQD 180
181 RLDCATAMHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGL 240
185 RLDCATAMHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGL 244
241 EINARDREGDTALHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTRHAL 300
245 EINARDREGDTALHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTRHAL 304
301 EHPEPGAHEHNGLEPNDSGRETPQVPAQ 329
305 EHPEPGAHEHNGLEPNDSGRETPQVPAQ 333

RESULT 3
Q9TU71 PRELIMINARY; PRT; 319 AA.
AC Q9TU71;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CARP.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20011295; PubMed-10542334;
RA Aihara Y., Kurabayashi M., Arai M., Kedes L., Nagai R.;
RT "Molecular cloning of rabbit CARP cDNA and its regulated expression in adriamycin-cardiomyopathy."
RL Blochim. Biophys. Acta 1447:318-324(1999).
DR EMBL; AF131883; AAF13817.1; -
DR HSP; Q00421; IAWC.
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 4.
DR SMART; SM00248; ANK; 4.
DR PROSITE; PS50088; ANK_REPEAT; 4.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR SEQUENCE 319 AA; 36245 MW; C7EF87A02936FED3 CRC64;

Query Match 40.0%; Score 677; DB 6; Length 319;
Best Local Similarity 46.4%; Pred. No. 3.2e-39;
Matches 136; Conservative 54; Mismatches 69; Indels 34; Gaps 3;

QY 29 GDTROKLPMDLVLEDEKHHGAQSAALQKVGQF-----RV 64
DB 18 GETGEFLP-----DDFRDQYEAATSEKQEDKLTPLAHVSLAEQOWEREKQLEAEL 70
QY 65 RKTSLDLRREIDYGGIONLIELKKRQKRDALAAASHPEEITGPVDEETFLKA 124
DB 71 KKKLEQRKLENLEDEEIIQLKKRKRKTKVPVAK-----PEPELITEPVDVPFLKA 127
QY 125 AVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDC 184
DB 128 ALENKLVAVKFLSDNNPDVCEYKRTALHRACLEGLAIVEKLMGAGQIEFRDML 187
QY 185 TAMHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGLEINA 244
DB 188 TAIHWACRGHLEVVVKLLSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFSLGLEINA 247
QY 245 RREGDTALHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTR 297
DB 248 KOREGDTPLHDVRLNRYKIILLLHGADMTKNLAGKTPDVLVOLWQADTR 300

RESULT 4
Q9Z1F0 PRELIMINARY; PRT; 319 AA.
ID Q9Z1F0

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Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 Suetani H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK009959: BAB26611.1;
 DR EMBL: AK009655: BAB26419.1;
 DR MGD: MGI:109621; ALP;
 DR InterPro: IPR002110; ANK.
 DR Pfam: PF00023; ank; 4.
 DR SMART: SM00248; ANK; 4.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
 SQ SEQUENCE 319 AA; 36003 MW; 26A3C4062CF0E7D0 CRC64;

Query Match 39.3%; Score 666; DB 11; Length 319;
 Best Local Similarity 47.7%; Pred. No. 1.8e-38;
 Matches 132; Conservative 54; Mismatches 77; Indels 14; Gaps 3;

QY 45 EKHHGAQSAALQKV-GEER-----VRKTSLDRLREIIVGGIQLKRRKQ 93
 DB 40 EKQEDKTLFANSVKGEQKSEKLEAELEKLEQSKLENLEDEIIVOLKRRKY 99
 QY 94 KKRDLAASHEPPPEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDFRRTA 153
 DB 100 KTKVPVVKVE---PEPEITPVDVPRFLAALNKLPVVEKFLSKNSPDVCEYKRTA 156
 QY 154 LHRASLEGHMEILKLDNGATVDFQDRDLCTAMHWACRGHLEVVKLLQSHGADTNVRD 213
 DB 157 LHRACLEGLAIVEKLEAGAEIIFRDLMELESTAHWACRGADNVLKLLNKGAKISARD 216
 QY 214 KLLSLPLHVAVTGVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLHGA 273
 DB 217 KLLSLHVAVTGVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLHGA 276
 QY 274 DMWTKNLAKGTPDILVOLWQADTRHLEHPEPGAHN 310
 DB 277 DLKVNKACGKTPMDLVLHWQSGTAFDLSLKENAYKN 313

RESULT 7
 ID Q15327 PRELIMINARY; PRT; 319 AA.
 AC Q15327;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE NUCLEAR PROTEIN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKIN;
 RX MEDLINE=95247734; PubMed=7730328;
 CHU W., Burns D.K., Swerlick R.A., Presky D.H.;
 RT "Identification and characterization of a novel cytokine-inducible
 RT nuclear protein from human endothelial cells.";
 RL J. Biol. Chem. 270:10236-10245(1995).
 DR EMBL: X83703; CAA58676.1;
 DR HSSP: Q00421; IAWC.
 DR InterPro: IPR002110; ANK.
 DR Pfam: PF00023; ank; 4.
 DR SMART: SM00248; ANK; 4.
 DR PROSITE: PS50088; ANK_REPEAT; 4.
 DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
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Query Match 39.9%; Score 658; DB 4; Length 319;
 Best Local Similarity 51.8%; Pred. No. 6.5e-38;
 Matches 129; Conservative 50; Mismatches 66; Indels 4; Gaps 2;
 QY 49 GAQSAALQKVGOERVKTSLDRLREIIVGGIQLKRRKQKRDALAAASHEPPPE 108
 DB 56 GEQQWKSQKREAE-LPEKKLEQSKLENLEDEIIVOLKRRKYRTPVVKVE---PE 111
 QY 109 PEETGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRSLEGHMEILEK 168
 DB 112 PEIITEPVDPVTPFLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRSLEGHMEILEK 171
 QY 169 LLDNGATVDFQDRDLCTAMHWACRGHLEVVKLLQSHGADTNVRDRLSLPLHVAVTGQ 228
 DB 172 LMEAGAQIEFRDLMELESTAHWASRGNDVLKLLNKGAKISARDKLLSLHVAVTG 231
 QY 229 VEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLHGAADMMTKNACKTPTDL 288
 DB 232 YECAEHLIACEADLNARDREGDTPLHDVRLNRYKIIKLLHGAADMMTKNACKTPTDL 291
 QY 289 VQLWQADTR 297
 DB 292 VLHWQNGTK 300

RESULT 8
 ID Q9NQC9 PRELIMINARY; PRT; 102 AA.
 AC Q9NQC9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE ANKYRIN REPEAT DOMAIN 2 (FRAGMENT).
 GN ANKRD2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SKELETAL MUSCLE;
 RX MEDLINE=20334618; PubMed=10873377;
 RA Kemp T.J., Sadusky T.G., Saltisi F., Carey N., Moss J., Yang S.Y.,
 RA Sassoon D.A., Goldspink G., Coulton G.R.;
 RT "Identification of Ankrd2, a novel skeletal muscle gene coding for a
 RT stretch-responsive ankyrin-repeat protein.";
 RL Genomics 66:229-241(2000).
 DR EMBL: AJ249975; CAB95416.1;
 FT NON_TER 1
 FT NON_TER 102
 FT NON_TER 102
 SQ SEQUENCE 102 AA; 11633 MW; 8DFD34CDCB44D1E5 CRC64;

Query Match 29.8%; Score 505; DB 4; Length 102;
 Best Local Similarity 29.0%; Pred. No. 5.4e-28;
 Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 19 AQEENEKLRGDTROKLPMDLLVLEDEKHGQAQSAALQKVGOERVKTSLDRLREIIV 78
 DB 2 AQEENEKLRGDTROKLPMDLLVLEDEKHGQAQSAALQKVGOERVKTSLDRLREIIV 61
 QY 79 GGTONLIELKRRKQKRDALAAASHEPPPEITGPVDEE 119
 DB 62 GGTONLIELKRRKQKRDALAAASHEPPPEITGPVDEE 102

RESULT 9
 ID Q9VUX2 PRELIMINARY; PRT; 1214 AA.
 AC Q9VUX2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

QY 195 HLEVVKLQSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFLSLGLEINARDREGDTALH 254
DB 696 RVSVVEYLHGHGADHAKDGLPLHNCASGYHVEAELLVRHGASVNVADLWKFTPLH 755
QY 255 DAVRLNRYKIILKLLHGHGADMTNKLAKTPTDLVLQWQADTRALE 301
DB 756 EAAAGKYEICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLLK 802
RESULT 11
Q9N043 PRELIMINARY; PRT; 307 AA.
ID Q9N043
AC Q9N043
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE UNNAMED PROTEIN PRODUCT.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
SUzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries."
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046089; BAB01671.1;
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 7.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 6.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
SQ SEQUENCE 307 AA; 35684 MW; D8E6EF1994504B95 CRC64;
Query Match 14.7%; Score 248.5; DB 6; Length 307;
Best Local Similarity 31.0%; Pred. No. 1.1e-09;
Matches 61; Conservative 32; Mismatches 71; Indels 33; Gaps 1;
QY 124 RAVEKMKVIEKFLADGSSADTCDFRRTALHRSLEHMEILEKLDNGATVDFO-- 181
DB 49 AANKGLPVPVILLKAGCDLVQDGDGTALHRAVTVGVNTEIIAALIHGCGALDRDRG 108
QY 182 -----LDCTAMHWACRGHLEVVKLQSHGADTN 210
DB 109 NTALEASWHGFSQAKLLVKGANVLAKNAGNTALHLAGNSHOSSTRVLLLAGSRAD 168
QY 211 VRDKLLSTPLHVAVRTGOVEIVEHFLSLGLEINARDREGDTALHRAVRLNRYKIILKLL 270
DB 169 LKNNAGDTCCLHVAARYNHLISIRLLLSAFCSVHEKQAGDTHALIAALNKKVAKILLE 228
QY 271 HGADMTNKLAKTPTD 287
DB 229 AGADTTIVNAGOTPLE 245
RESULT 12
Q9LQF7 PRELIMINARY; PRT; 543 AA.
ID Q9LQF7
AC Q9LQF7
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE F24B9.19 PROTEIN.
GN F24B9.19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Liu S., Yu G., Sakano H., Jhaveri A., Lee J., Lenz C., Pham P.,
RA Toriumi M., Chin C., Choi E., Chlou J., Gonzalez A., Chung M.,
RA Howing B., Koo T., Li J., Liu A., Vaysberg M., Altafi H., Brooks S.,
RA Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.,
RA Johnson-Hopson C., Khan S., Kim C., Lam B., Nguyen M., Palm C.,
RA Shin P., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "The sequence of BAC F24B9 from Arabidopsis thaliana chromosome 1."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis A.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Theologis;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC007583; AAF7503.1;
DR InterPro; IPR002110; ANK.
DR Pfam; PF00023; ank; 8.
DR SMART; SM00248; ANK; 6.
DR PROSITE; PS50088; ANK_REPEAT; 6.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
SQ SEQUENCE 543 AA; 58911 MW; C06C4C1B9E271DC8 CRC64;
Query Match 14.6%; Score 247.5; DB 10; Length 543;
Best Local Similarity 29.1%; Pred. No. 2.6e-09;
Matches 102; Conservative 48; Mismatches 121; Indels 79; Gaps 15;
QY 21 EEENEKLRGDTROKLPK-----DLLVLEDEKHHG-----AQSAALQKVGK- 60
DB 2 EGEEDTVAGSSIPKMKMKQUTGKRDDTLHSAVRHGNKDRVVEILTKTRESLNQLLKG 61
QY 61 QERVKTSILDRRELIIDYGGION-----LIELRKRRKKOKKRDALAAASHEPPPEPEI 112
DB 62 QNQSGETALYVAEYGVDEIVKEMINCYDLALVEI-----KARNGFDAFH----- 106
QY 113 TGPVDEETFLKAABEGKMKVIEKFLADGGS--ADTCDFRRTALHRSLEHMEILEKLL 170
DB 107 -----IAAKQGDLDVL-KVLAEAHSELAMTVDSLNTALHTAATQGHTEVNFLL 155
QY 171 DNGATV-DFQDRLDCTAMHWACRGHLEVVK-LLOSHGADTNVRDKLLSTPLHVAVRTGO 228
DB 156 ELGSSLIAGTAKNGKTAHLSASRNGHVYKALLASEPAIAIRMDKKGQTAHLMVAKGTN 215
QY 229 VEIVEHFLSLG-LEINARDREGDTALHRAVRLNRYKIILKLLHG-ADMTNKLAKTPT 286
DB 216 VEVVEELIKADRSSINIAITKNTALHIAARKRSQIVKLLANNMTDTKAVNRSGE-- 273
QY 287 DLVQLWQADTRHALEHPE-----FGAEHNGLEGPNDSGRETPQPV 326
DB 274 -----ALDTAEKIGNPEVALIILQKHGVSFAKTIKPSGNPA-RELKQTV 316
RESULT 13
Q9H2K2 PRELIMINARY; PRT; 1166 AA.
ID Q9H2K2
AC Q9H2K2
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE TANKYRASE-LIKE PROTEIN (TANKYRASE 2).

GN TNKL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST CARCINOMA;
RA Kaimov A.N., Kuprash D.V., Petrov V.N., Vdovichenko K.K.,
RA Boitchenko V.E., Scanlan M.J., Jongeneel C.V., Nedospasov S.A.,
RA Lagarkova M.A.;
RT "Cloning and characterization of TNKL, a member of tankyrase/ankyrin
RT gene family.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kaminker P.G., Campisi J., Kim S.H., Yaswen P., Morin G.;
RT "Rapid induction of apoptosis by ectopic expression of TANK2, a novel
RT telomere-associated PARP.";
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Lyons R.J., Deane R., Lynch D.K., Ye Z.-S.J., Sanderson G.M.,
RA Eyre H.J., Sutherland G.R., Daly R.J.;
RT "Identification of a novel human tankyrase through its interaction
RT with the adaptor protein Grb14.";
J. Biol. Chem. 0:0-0(2001).
DR EMBL: AF264912; AAK4694.1;
DR EMBL: AF342982; AAK25811.1;
DR EMBL: AF329696; AAK13463.1;
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00023; ank; 16.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS50088; ANK_REPEAT; 15.
DR PROSITE: PS50297; ANK_REP_REGION; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR FT NON_TER 1
SQ SEQUENCE 1166 AA; 126917 MW; 4C8B38BD97CE704 CRC64;

Query Match 14.6%; Score 247.5; DB 4; Length 1166;
Best Local Similarity 23.4%; Pred. No. 6.7e-09;
Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;
Qy 34 NEKLGRDTRQKLPMDLLVLEDEKHHGAQSAALQKVGQERVKTS----LDLRRRIIDVG 79
Db 408 SEKAND-----VVEVVVHEAKVNALDNL-GOTSLHRAAYCGHLQTCRLLSYG 456
Qy 80 GIONLIELR-----KRRQKRRDALA-ASHEPPPEPEITGPVDEETFLK----- 123
Db 457 CDPNIISLQGTALQMGHNVQQLLEGISLGNSEADRLLEAAKAGDVETVKLCITVQS 516
Qy 124 -----AAVEGKMKVIERFLADGGSDTCDFRRTALHRSLEGHMEILE 167
Db 517 VNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDGGVPLHNAACSYGHEVAE 576
Qy 168 KLLDNGATVDFQDLDCDTAMHWACRGHLEVVKLLQSHGA-----D 208
Db 577 LLVKGAVNVNADLWKFTPLHEAAKGYEICKLLQHGADPTKKNRGNTPLDLVKDGD 636
Qy 209 TNVRDKLL-----STPLHVAVRTGOVEIVE 233
Db 637 TDIDQLLRGDAALLDAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAE 696
Qy 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
Db 697 YLLQHGADVNAQDKGLPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKG 756
Qy 261 RYKIILKLLLLHGADMTNLAGKTPTDLVQWQADTRHAL-----EHPE--- 304

Db 757 RTQCLALLAHGADPTLKNQEGQTPDLV-----SADDVSALLTAAMPSPALPSCYKPOVLN 813
Qy 305 ----PGAEHNGLEGPNDSGRETPQPVPA 328
Db 814 GVRSPGATADAL-----SSGPPSPSSLSA 837
RESULT 14
Q9HAS4
ID Q9HAS4 PRELIMINARY; PRT; 1265 AA.
AC Q9HAS4;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE TANKYRASE-RELATED PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Mor: D.W., Meese E.;
RT "Novel tankyrase-related gene.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF305081; AAG25674.1;
DR InterPro: IPR002110; ANK.
DR InterPro: IPR000345; CytC_heme_bind.
DR InterPro: IPR001660; SAM.
DR Pfam: PF00023; ank; 16.
DR Pfam: PF00536; SAM; 1.
DR PRINTS: PR01415; ANKYRIN.
DR SMART: SM00248; ANK; 15.
DR SMART: SM00454; SAM; 1.
DR PROSITE: PS50088; ANK_REPEAT; 15.
DR PROSITE: PS50297; ANK_REP_REGION; 1.
DR PROSITE: PS00190; CYTOCHROME_C; UNKNOWN_1.
DR FT NON_TER 1
SQ SEQUENCE 1265 AA; 136905 MW; 3BFD7DE7AEBC038 CRC64;

Query Match 14.6%; Score 247.5; DB 4; Length 1265;
Best Local Similarity 23.4%; Pred. No. 7.5e-09;
Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;
Qy 24 NEKLGRDTRQKLPMDLLVLEDEKHHGAQSAALQKVGQERVKTS----LDLRRRIIDVG 79
Db 507 SEKAND-----VVEVVVHEAKVNALDNL-GOTSLHRAAYCGHLQTCRLLSYG 555
Qy 80 GIONLIELR-----KRRQKRRDALA-ASHEPPPEPEITGPVDEETFLK----- 123
Db 556 CDPNIISLQGTALQMGHNVQQLLEGISLGNSEADRLLEAAKAGDVETVKLCITVQS 615
Qy 124 -----AAVEGKMKVIERFLADGGSDTCDFRRTALHRSLEGHMEILE 167
Db 616 VNCRDIEGRQSTPLHFAAGYNRVSVVEYLLQHGADVHAKDGGVPLHNAACSYGHEVAE 675
Qy 168 KLLDNGATVDFQDLDCDTAMHWACRGHLEVVKLLQSHGA-----D 208
Db 676 LLVKGAVNVNADLWKFTPLHEAAKGYEICKLLQHGADPTKKNRGNTPLDLVKDGD 735
Qy 209 TNVRDKLL-----STPLHVAVRTGOVEIVE 233
Db 736 TDIDQLLRGDAALLDAKKGCLARVKKLSSPDNVNCRDTQGRHSTPLHLAAGYNNLEVAE 795
Qy 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
Db 796 YLLQHGADVNAQDKGLPLHNAASYGHVDVAALLIKYNACVNATDKWAFPLHEAAQKG 855
Qy 261 RYKIILKLLLLHGADMTNLAGKTPTDLVQWQADTRHAL-----EHPE--- 304
Db 856 RTQCLALLAHGADPTLKNQEGQTPDLV-----SADDVSALLTAAMPSPALPSCYKPOVLN 912

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QY 305 ----PGAENHGLEGNDSGRETPQVPA 328
DB 913 GVRSPGATADAL-----SSGPSSPSSLSA 936

RESULT 15
Q9H01A
ID Q9H01A PRELIMINARY; PRT; 1050 AA.
AC Q9H01A;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TRENBLrel. 17, Last annotation update)
DE HYPOTHETICAL 117.0 KDA PROTEIN.
GN DKFZP434L0718.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL136784; CAB66718.1;
DR InterPro; IPR002110; ANK.
DR InterPro; IPR003123; VPS9.
DR Pfam; PF00023; ank; 8.
DR Pfam; PF02204; VPS9; 1.
DR PRINTS; PR01415; ANKYRIN.
DR SMART; SM00248; ANK; 8.
DR SMART; SM00167; VPS9; 1.
DR PROSITE; PS50088; ANK_REPEAT; 8.
DR PROSITE; PS50297; ANK_REPEAT; 1.
KW Hypothetical protein.
SQ SEQUENCE 1050 AA; 117012 MW; 6A0D4F77F3C1D11D CRC64;

Query Match 14.4%; Score 244; DB 4; Length 1050;
Best Local Similarity 25.6%; Pred. No. 1e-08;
Matches 87; Conservative 46; Mismatches 117; Indels 90; Gaps 10;

QY 24 NEKLRGDTROKLPMDLL-----VLEDEKHGAQSAALQKVGQERVKTSLD--LRRE 74
DB 562 NEK--GDT---PLHIAARWGQYGVETLLQNGASTEI-----QNLKETPLKCALNSK 609
QY 75 IIDVGGIQNLIELRKKOKKRDALAAASHEPPPEPEIT-----GPVDEET- 120
DB 610 ILSV---WEAYHLSFERRQKSSSEAPVQS--PQRSVDSISQESSTSFSSMSAGSRQETK 664
QY 121 -----FLKAAVEGKMKVIEKFL----- 137
DB 665 KDYREVEKLLRAVADGDLEMYRYLLEWTEDEDAEDTVSAADPEFCHPLCQCPKCAPAQ 724
Y 138 -----ADGGSADTCQFRTALHRASLEGHMEILEKLLDNGATVDFDRLDCTAMHWA 190
DB 725 KRLAKVPASGLGVNVTSDGSSPLHVAALHGRADLIRLLKHLKHGAGARNADQAVPLHLA 784
QY 191 CRGGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEINARDREGD 250
DB 785 COQGHFQVVKLLDSNAKPNKKDLGNTPLIYACSGGHHVALLLQHGASINASNKNKN 844
QY 251 TALHDAVRLNRYKIKLLHGHADMMTKNLAKGTPDVLQ 290
DB 845 TALHEAVIEKHVFVVELLLHGHASVQVNLNKRORTAVDCAE 884
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:09:42 ; Search time 23.95 Seconds
(without alignments)
1017.541 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /SID88/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SID88/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SID88/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SID88/gcgdata/geneseq/geneseq/AA1985.DAT:*

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1688	99.7	329	22	Human polypeptide
2	892	52.7	182	22	Human polypeptide
3	658	38.9	319	22	Human shear stress
4	296.5	17.5	510	22	Human polypeptide
5	282.5	16.7	978	21	Human OREF ORF2052
6	249.5	14.7	949	21	Human truncated ta
7	249.5	14.7	1327	21	Human tankyrase I
8	249.5	14.7	1327	21	Human tankyrase
9	249.5	14.7	1327	22	Human tankyrase I
10	248	14.6	1166	22	Human SPANK. Homo
11	247.5	14.6	784	22	Human tankyrase2 c

12	247.5	14.6	1074	20	Human Grb7 effecto
13	247.5	14.6	1100	22	Tankyrase homology
14	247.5	14.6	1166	21	Human tankyrase II
15	247.5	14.6	1166	22	Human tankyrase2 T
16	247.5	14.6	1169	22	Human tankyrase2 I
17	247.5	14.6	1169	22	Human tankyrase2 c
18	247.5	14.6	1240	22	Tankyrase homology
19	247.5	14.6	1262	22	Human tankyrase2 c
20	247.5	14.6	1385	22	Human tankyrase2 T
21	246.5	14.6	756	22	Human tankyrase2 c
22	246	14.5	991	22	Mouse SPANK. Mus
23	245.5	14.5	907	22	Human breast cance
24	244	14.4	1166	22	Human tankyrase ho
25	240.5	14.2	868	21	Arabidopsis thalia
26	240.5	14.2	879	21	Arabidopsis thalia
27	240.5	14.2	890	21	Arabidopsis thalia
28	237.5	14.0	522	22	Human tankyrase2 c
29	235	13.9	551	22	Human death domain
30	235	13.9	1715	22	Human polypeptide
31	235	13.9	1715	22	Human polypeptide
32	233	13.8	765	22	Human protein kina
33	231	13.6	1181	22	Drosophila tankyra
34	230.5	13.6	362	22	Human TRF1 TANK2 b
35	230.5	13.6	840	22	Human polypeptide
36	230	13.6	705	22	Human colon cancer
37	228	13.5	1088	22	Human kidney ankyr
38	228	13.5	1333	21	Human tankyrase II
39	224	13.2	679	15	2-5A-dependent RNA
40	224	13.2	679	16	Partial murine 2-5
41	224	13.2	679	18	Mouse 2-5A-depende
42	224	13.2	679	20	Mouse 2-5A-depende
43	223	13.2	422	15	Fowlpox virus (FPV
44	223	13.2	422	15	Fowlpox virus prot
45	223	13.2	422	18	Homology vector 44

ALIGNMENTS

RESULT 1
AAM40353
ID AAM40353 standard; Protein; 329 AA.

AC AAM40353;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 3498.

Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
peripheral nervous system; neuropathy; central nervous system; CNS;
Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

OS Homo sapiens.

PN WO200153312-A1.

PD 26-JUL-2001.

PF 26-DEC-2000; 2000WO-US34263.

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

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QY 124 AAVEGKMKVTEKFLADGSGADTCDFRRFALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
 Db 27 aanaavkcaevliplssvvnvsgrrtalhaaanghgvemvlllkganinatdkkd 86
 QY 184 CTAMHACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFLSLGLEIN 243
 Db 87 rralhwaaymgldvallinhgaevctckdkgytphaaasngvnnvkhlinlgveid 146
 QY 244 ARDREGDTALHDVAVRLNRYKIIKLLHGDGMTKLAGTPTDVLQWQADTRHAL 300
 Db 147 einvyngntalhiacynggdavvnvnelidyanvnpnnngftp---lnfaaasthgal 200

RESULT 5
 AAB42286
 ID AAB42288 standard; Protein: 978 AA.
 XX AC AAB42288;
 XX DT 08-FEB-2001 (first entry)
 XX DE Human ORFX ORF2052 polypeptide sequence SEQ ID NO:4104.
 XX KW Human: open reading frame; ORFX: detection; cytotatic; hepatotropic;
 XX KW vulnary; antipariatic; antiparkinsonian; nootropic; neuroprotective;
 XX KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 XX KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 XX KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 XX KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 XX KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 XX KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 XX KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 XX KW cholesterol ester storage; systemic lupus erythematosus; infection;
 XX KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 XX KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 XX KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 XX KW thrombosis; contraceptive.

OS Homo sapiens.
 XX WO200058473-A2.
 XX PD 05-OCT-2000.
 XX PF 31-MAR-2000; 2000WO-US08621.
 XX PR 31-MAR-1999; 99US-0127607.
 XX PR 02-APR-1999; 99US-0127636.
 XX PR 05-APR-1999; 99US-0127728.
 XX PR 30-MAR-2000; 2000US-0540763.
 XX PA (CURA-) CURAGEN CORP.
 XX Shinkets RA, Leach M;
 DR WPI; 2000-602362/57.
 DR N-PSDB: AAC76497.
 XX Novel nucleic acids and peptides derived from open reading frame x,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 PS Claim 11; Page 3289-3292; 5507pp; English.
 XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytotatic; hepatotropic; vulnary;
 CC antipariatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteopathic; anticonvulsant; antithyroid; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antithyroid; and antianaemic. The sequences can be used for determining

CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 978 AA;

Query Match 16.7%; Score 282.5; DB 21; Length 978;
 Best Local Similarity 28.1%, Pred. No. 1.7e-18;
 Matches 94; Conservative 44; Mismatches 120; Indels 77; Gaps 9;

QY 28 RGDTRCKLPMDLLVLEDEK-----HGAOSAALQKVGQGVRYKTSLDLRREII 76
 Db 347 qpggketlesialidsekpkklrfhpqlyfsarqgelqkyl-----im 391
 QY 77 DVGGIONLIELKRRKQKRDALAAASHEPPPEETGPVD----- 117
 Db 392 lvdgldpnf---kmehqnkrspphaae-----aghvdichmlvqaganidtcseq 440
 QY 118 EEFFLKAAVEGKMKVIEKFLADGSGADTCDFRRFALHRASLEGHMEILEKLLDNG-ATV 176
 Db 441 rtplmeaennhleaavkylakagldvdpkdaegstclhlaakghyevvyllsngmrdv 500
 QY 177 DFQDRLDCTAMHACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIVEHFL 236
 Db 501 ncqddggwtpmiwaeykghvdlvklillskgsdinirneeniclhwafsgcvdiaeill 560
 QY 237 SLGLEINARDREGDTALHDVAVRLNRYKIIKLLHGDGMTKLAGTPTDVLV---QLW 292
 Db 561 aakcdlhaavnihgdsphlaaarenrydcvvlfsrdsdvtlknkegetplqcaslnsqw 620
 QY 293 QA-DTRHALEHPEPGAENGLEGNDSGRETPQPV 326
 Db 621 salqmskalq-----dsaprpapv 640

RESULT 6
 AAY44404
 ID AAY44404 standard; protein: 949 AA.
 XX AC AAY44404;
 XX DT 22-MAR-2000 (first entry)
 XX DE Human truncated tankyrase-2.
 XX KW Human tankyrase; TRF1; telomeric repeat binding factor-1;
 KW telomere length regulation; recombinant tankyrase; aging; skin atrophy;
 KW macular degeneration; atherosclerosis; ataxia telangiectasia;
 KW tankyrase modulator; rational drug design.
 OS Hemo sapiens.
 XX WC9964606-A1.
 XX PN 16-DEC-1999.
 XX PD 09-JUN-1999; 99WO-US12968.
 XX PR 10-JUN-1998; 98US-0095225.
 XX PR 17-AUG-1998; 98US-0135233.
 XX PR 19-NOV-1998; 98US-0196387.
 XX PA (BYRQ) UNIV ROCKEFELLER.

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ataxia telangiectasia; tankyrase modulator; rational drug design.

Homo sapiens.

Key Location/Qualifiers

Domain 181..1010

note="Ankyrin-specific (ANK) repeat consensus domain"

Domain 1023..1088

label="Sterile_alpha_motif"

Domain 1176..1314

note="Poly(ADP-ribose)polymerase (PARP) related domain"

WO9964606-A1.

16-DEC-1999.

09-JUN-1999; 99WO-US12968.

10-JUN-1998; 98US-0095225.

17-AUG-1998; 98US-0135233.

19-NOV-1998; 98US-0196387.

(UYRQ) UNIV ROCKEFELLER.

De Lange T, Smith S;

WPI: 2000-116549/10.

N-PSDB; AA229627.

New nucleic acid encoding vertebrate tankyrase, a regulator of telomere length, used to identify modulators, e.g. for inhibiting growth of cancer

- Claim 1; Fig 1B; 133pp; English.

The present sequence is human tankyrase, a TRF1 (telomeric repeat binding factor-1) binding protein. This was isolated using a two-hybrid screen with TRF1. Tankyrase is involved in regulation of telomere length through TRF1 and may directly modulate the effect of TRF1. Recombinant tankyrase, or its fragments are used to identify specific modulators which are potential drugs for countering telomere shortening associated with aging (e.g. atrophy of skin, macular degeneration or atherosclerosis) or diseases like ataxia telangiectasia. They are also used to raise specific antibodies (used as immunoassay reagents and as modulators of tankyrase activity) and in rational drug design.

Sequence 1327 AA;

Query Match 14.7%; Score 249.5; DB 21; Length 1327;

Best Local Similarity 26.2%; Pred. No. 4e-15;

Matches 91; Conservative 33; Mismatches 110; Indels 113; Gaps 9;

40 LVLEDEKH---HGAQSAALQKVGQERVKTSLDLRRIIDVGGION-----LIELR 88

484 ltyefkghslqqaeadlakvk-----kt---lalelnfkqpqshetalhcavaslh 534

89 KKRKQ-----KKRDALAAASHEPPPEEITGPVDEETFLKAAVEGKMKVIE 134

535 pkrkqvteillrrkganvneknkdfmtplh-----vaaerahndvme 575

135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNG----- 173

576 vlkhgkmmaldtlgqthalhraalaghiqtrclllsygsdpsiiislggftaaqmgneav 635

174 -----ATVDFQ-----DRLDC-----TAMHWACRGG 194

636 qqilsestprtssdvyrllleaskagdlctvklcqqnqncrdleghrstplhfaagyn 695

195 HLEVYKLLQSHGADTNVRDKLLSTPLHVAVRTQGVIEFHSLSGLEINAREGDTALH 254

696 rvsveyllhhgadvhakdgkigvplhnacsyghyevaelvrrhgasvnnvadlwktfplh 755

255 DAVRLNRYKIILKLLHGGADMMTKNLAGKTPDILVQLWQADTRHALE 301

756 eaaakgyeicklilkngadptknrdgntpldivkegdtidqllk 802

RESULT 9

AA66279

ID AAB66279 standard; Protein; 1327 AA.

XX AAB66279;

XX 05-APR-2001 (first entry)

XX Human tankyrase1 SEQ ID NO: 4.

XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging; inflammatory disorder.

XX Homo sapiens.

XX WO200100849-A1.

XX 04-JAN-2001.

XX 28-JUN-2000; 2000WO-US17827.

XX 29-JUN-1999; 99US-0141582.

XX (ICOS-) ICOS CORP.

XX Christenson E, Demaggio AJ, Goldman PS, McElligott DL;

XX WPI: 2001-102896/11.

XX N-PSDB; AAF63838.

XX New tankyrase2 polypeptides, useful for treating conditions mediated by poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers, inflammatory and autoimmune disorders

XX Example 1; Page 118-121; 242pp; English.

The present invention provides the protein and coding sequence for the human tankyrase2 protein. This is found in two different versions, designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has polyADP-ribosylation activity and is involved in the modification of TRF1, which is a telomere-specific binding protein. The regulation of telomere length, in which TRF1 has a role, is linked to ageing and cancer. The sequences are useful in the treatment of cancers and inflammatory disorders.

Sequence 1327 AA;

Query Match 14.7%; Score 249.5; DB 22; Length 1327;

Best Local Similarity 26.2%; Pred. No. 4e-15;

Matches 91; Conservative 33; Mismatches 110; Indels 113; Gaps 9;

40 LVLEDEKH---HGAQSAALQKVGQERVKTSLDLRRIIDVGGION-----LIELR 88

484 ltyefkghslqqaeadlakvk-----kt---lalelnfkqpqshetalhcavaslh 534

89 KKRKQ-----KKRDALAAASHEPPPEEITGPVDEETFLKAAVEGKMKVIE 134

535 pkrkqvteillrrkganvneknkdfmtplh-----vaaerahndvme 575

135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNG----- 173

576 vlkhgkmmaldtlgqthalhraalaghiqtrclllsygsdpsiiislggftaaqmgneav 635

174 -----ATVDFQ-----DRLDC-----TAMHWACRGG 194

636 qqilsestprtssdvyrllleaskagdlctvklcqqnqncrdleghrstplhfaagyn 695

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PI Christenson E, Demaggio AJ, Goldman PS, McElligott DL;
 XX WPI; 2001-102896/11.
 DR N-PSDB; AAF63917.
 XX
 XX New tankyrase2 polypeptides, useful for treating conditions mediated by
 PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
 PT inflammatory and autoimmune disorders.
 XX
 XX Example 1; Page 144-146; 242pp; English.
 XX
 XX The present invention provides the protein and coding sequence for the
 XX human tankyrase2 protein. This is found in two different versions,
 CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has
 CC polyADP-ribosylation activity and is involved in the modification of
 CC TRF1, which is a telomere-specific binding protein. The regulation of
 CC telomere length, in which TRF1 has a role, is linked to ageing and
 CC cancer. The sequences are useful in the treatment of cancers and
 CC inflammatory disorders.
 XX
 XX Sequence 784 AA;

Query Match 14.6%; Score 247.5; DB 22; Length 784;
 Best Local Similarity 23.4%; Pred. No. 3.1e-15;
 Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;

QY 24 NEKLGRDTRQKLPMDLLVLEDEKHHGAQSAALQKVGQERVKTS-----LDLREIIVDG 79
 Db 26 sekahnd-----vvevvvkhakvndnl-gqtslhraaycghlqtrlllsyg 74
 QY 80 GIONLIELR-----KKRQKKRDALA-ASHEPPPEPEITGPVDETEFLK----- 123
 Db 75 cdpniislgftalqmgnevvqllqegisignseadrqlleaakagdvctvklctvqs 134
 QY 124 -----AAVEGKMKVIEKFLADGGSADTCDFRRRTALHRASLEGHMEILE 167
 Db 135 vncrdiegrstplhfaagynrvsvveyllqhgadvhdkdggglvplhnacsyghyevae 194
 QY 168 KLLDNGATVDFQRLDCTAMHWACRGHLEVVKLQSHGA-----D 208
 Db 195 llvkhgavnnvadlwkftplheaakgkyeicklllqhgadptkknrdgntpldivkdg 254
 QY 209 TNVRDKLL-----STPLHAVRTGOVEIVE 233
 Db 255 tdigqlrgdaalldaakgclarvkkllsspdnvnrcdtggrhstplhlaagynnlvae 314
 QY 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
 Db 315 yllqhgadvnagdkgglplhnaasyghdvaaallkynacvnatdkwaftplheaakg 374
 QY 261 RYKIIKLLLLHAGDMWTKNLAKGTPDVLQWQADTRHAL-----EHPE--- 304
 Db 375 rtqicallahgadptlknqgqtpdliv---saddvsalltaampspalpcykpgvln 431
 QY 305 -----PGAENHLEGNDSGRETQPQVPA 328
 Db 432 gvrspgataal-----ssgspsspslsa 455

RESULT 12
 AAY05734
 ID AAY05734 standard; Protein; 1074 AA.
 XX
 AC AAY05734;
 XX
 DT 19-JUL-1999 (first entry)
 XX Human Grb7 effector 2.2412 protein.
 DE
 XX Grb7 effector; 2.2412 protein; human; signal transduction;
 KW tumour marker; breast cancer; prostate cancer; prognosis;
 KW diagnosis.

XX Homo sapiens.
 OS
 XX W09915647-A1.
 PN
 XX 01-APR-1999.
 PD
 XX 23-SEP-1998; 98WO-AU00795.
 PF
 XX 23-SEP-1997; 97AU-0009388.
 PR
 XX (GAEV-) GARVAN INST MEDICAL RES.
 PA
 XX Daly RJ, Sutherland RE;
 XX WPI: 1999-254707/21.
 DR N-PSDB; AAX25366.
 XX
 XX New candidate effector for the Grb7 family of signaling proteins,
 PT and specific antibody, useful for detection and treatment of cancer
 PT
 XX
 XX Claim 9; Fig 1; 24pp; English.
 XX
 XX The present sequence represents a novel candidate effector for
 CC the Grb7 family of signalling proteins, termed 2.2412. The
 CC sequence is predicted from a partial cDNA (see AAX25366). 2.2412
 CC mRNA transcripts (7 kb) were detected in all tissues examined
 CC with the exception of kidney. Expression was particularly high in
 CC skeletal muscle and placenta. Analysis of the sequence revealed
 CC significant homology to a large number of proteins containing
 CC ankyrin-like repeats. The 2.2412 gene was localised to between
 CC chromosome 10q23.2 and proximal 10q23.32. Deletions in the
 CC 10q22-25 region have been detected in human breast, prostate,
 CC renal, small cell lung, and endometrial carcinomas, glioblastoma
 CC multiforme, melanoma and meningiomas. Detection of the protein
 CC encoded by the 2.2412 cDNA in a sample should provide a useful
 CC tumour marker and/or prognostic indicator for certain human
 CC cancers, in particular breast cancer and prostate cancer.
 CC Antagonism of the interaction between Grb7 family members and the
 CC encoded protein should provide a novel treatment strategy for human
 CC diseases exhibiting aberrant receptor tyrosine kinase signalling,
 CC such as cancer. Anti-Grb7 antibodies can be used in methods of
 CC detecting the presence of 2.2412 protein in a sample.
 XX
 XX Sequence 1074 AA;

Query Match 14.6%; Score 247.5; DB 20; Length 1074;
 Best Local Similarity 23.4%; Pred. No. 4.7e-15;
 Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;

QY 24 NEKLGRDTRQKLPMDLLVLEDEKHHGAQSAALQKVGQERVKTS-----LDLREIIVDG 79
 Db 316 sekahnd-----vvevvvkhakvndnl-gqtslhraaycghlqtrlllsyg 364
 QY 80 GIONLIELR-----KKRQKKRDALA-ASHEPPPEPEITGPVDETEFLK----- 123
 Db 365 cdpniislgftalqmgnevvqllqegisignseadrqlleaakagdvctvklctvqs 424
 QY 124 -----AAVEGKMKVIEKFLADGGSADTCDFRRRTALHRASLEGHMEILE 167
 Db 425 vncrdiegrstplhfaagynrvsvveyllqhgadvhdkdggglvplhnacsyghyevae 484
 QY 168 KLLDNGATVDFQRLDCTAMHWACRGHLEVVKLQSHGA-----D 208
 Db 485 llvkhgavnnvadlwkftplheaakgkyeicklllqhgadptkknrdgntpldivkdg 544
 QY 209 TNVRDKLL-----STPLHAVRTGOVEIVE 233
 Db 545 tdigqlrgdaalldaakgclarvkkllsspdnvnrcdtggrhstplhlaagynnlvae 604
 QY 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260

Db 605 yllqhgadnagdkggliplnhaasyghdvaaallikynaslnatdkwafplheaackg 664
Qy 261 RYKIILKLLHGGADMTKLNLAGKTPDLVQLWQADTRHAL-----EHPE--- 304
Db 665 rtqlcallangadptlknegqgtpdlv---saddvsalltaampspalpsckypqvl 721
Qy 305 ----PGAENHNGLEGNDSGRETPQVPVA 328
Db 722 gvrspgatal-----ssgppsspslsa 745

RESULT 13
AAY97748
ID AAY97748 standard; Protein; 1100 AA.
XX
XX AAY97748;
DT 06-AUG-2001 (first entry)
XX
XX Tankyrase homologue isotype 1 protein sequence.
XX
XX Tankyrase homologue isotype 1; TaHo-1; TaHo-2; cell proliferation;
KW cell cycle protein; cell cycle associated disorder; cancer; gene mapping;
KW chromosome mapping; gene therapy; vaccine.
XX Unidentified.
XX WO200130987-A2.
XX
XX 03-MAY-2001.
XX
XX -25-OCT-2000; 2000WO-US41528.
XX
XX 25-OCT-1999; 99US-0427154.
XX
XX (RIGE-) RIGEL PHARM INC.
XX
XX Luo Y, Chan E, Xu X, Huang B;
XX
XX WPI: 2001-300503/31.
XX N-PSDB; AAA91487.
XX
XX Novel recombinant cell cycle polypeptide, tankyrase H useful for
XX inducing or preventing cell proliferation in cells, and for diagnosing,
XX treating or preventing cell cycle associated disorders such as cancer
XX
XX Claim 22; Fig 3; 63pp; English.
XX
XX This sequence is the Tankyrase homologue isotype 1 (TaHo-1) protein
XX of the invention. The invention also relates to the TaHo-2 protein.
XX The TaHo proteins are useful for inducing or preventing cell
XX proliferation in cells, and in the study or treatment of conditions
XX mediated by the cell cycle proteins, such as to diagnose, treat or
XX prevent cell cycle associated disorders, preferably cancer. The TaHo
XX coding sequences are useful as hybridisation probes, in chromosome and
XX gene mapping and in the generation of anti-sense DNA and RNA. The coding
XX sequences are also useful for the preparation of TaHo, for generating
XX either transgenic animals or knock out animals which, in turn, are useful
XX in a development and screening of therapeutically useful agents, in gene
XX therapy, as vaccine, and for construction of hybridisation probes for
XX mapping the gene which encodes TaHo and for the genetic analysis of
XX individuals with genetic disorders. The TaHo proteins, and their coding
XX sequences are useful in screening assays.
XX
XX Sequence 1100 AA;
SQ

Query Match 14.6%; Score 247.5; DB 22; Length 1100;
Best Local Similarity 23.4%; Pred. No. 4.9e-15;
Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;
Qy 24 NEKRGDTRQKLPMDDLLEDEKHHGAQSAALQKVGQERVRKTS-----LDLRRREIIDVG 79

Db 342 sekahnd-----vvevvvkheakvnaIdnl-gqtslhraaycghlqtcrlilsyg 390
Qy 80 GIONLIELR-----KKRQKKRDALA-ASHEPPEPEPEITGPVDEETFLK----- 123
Db 391 cdpnlislgftalqmgngenvqllqegislgneadqrllleaakagdvettvkktctvqs 450
Qy 124 -----AAVEGKMKVIEFLADGGSDATCDQFRRTALHRALESIGHEMEILE 167
Db 451 vncrdiegrqstplhfaagynrvsvveyllqhgadvhakdkgglvplhnacsyghyvae 510
Qy 168 KLLNGATVDFQDLDCDTAMHWACRGHLEVVKLLQSHGA-----D 208
Db 511 llvkhgavvnvadiwkftplheaakgkycicklllqhgadptlknrdgntpldlvkdg 570
Qy 209 TNVRDKLL-----STPLHVAVRTGOVEIVE 233
Db 571 tdigdlirgdaalldaakkgclarvkkisspndvncrdtqgrhscplhlaagynnievae 630
Qy 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
Db 631 yllqhgadnagdkggliplnhaasyghdvaaallikynacvnatdkwafplheaackg 690
Qy 261 RYKIILKLLHGGADMTKLNLAGKTPDLVQLWQADTRHAL-----EHPE--- 304
Db 691 rtqlcallangadptlknegqgtpdlv---saddvsalltaampspalpsckypqvl 747
Qy 305 ----PGAENHNGLEGNDSGRETPQVPVA 328
Db 748 gvrspgatal-----ssgppsspslsa 771

RESULT 14
AAB27211
ID AAB27211 standard; Protein; 1166 AA.
XX
XX AAB27211;
DT 27-FEB-2001 (first entry)
XX
XX Human tankyrase II protein sequence SEQ ID NO: 6.
XX
XX Human; tankyrase II; telomere length; signal transduction.
KW
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 124 /note= "encoded by TTA"
FT Misc-difference 125 /note= "encoded by TAC"
XX
XX WO2000061813-Al.
XX
XX 19-OCT-2000.
XX
XX 10-APR-2000; 2000WO-US09558.
XX
XX 09-APR-1999; 99US-0128577.
XX 13-APR-1999; 99US-0129123.
XX
XX (GERO-) GERON CORP.
PI Morin GB, Funk WD, Piatyszek MA;
XX
XX WPI: 2000-679503/66.
XX N-PSDB; AAC66825.
XX
XX Novel mammalian Tankyrase II polypeptide and the polynucleotide
XX encoding the polypeptide useful for modulating or maintaining telomere
XX length, replicative capacity, apoptosis, chromosome packing or gene
XX expression

Claim 4; Fig 4; 52pp; English.

XX The present sequence is a version of the human tankyrase II protein
 CC sequence. The protein is thought to be involved in signal transduction in
 CC the cell, and to have binding activity for other telomere-associated
 CC proteins. It is possible that it plays a role in the regulation of
 CC telomere length, thus affecting the replicative ability of the cell. The
 CC protein is useful for ribosylating target proteins, for determining
 CC tankyrase II binding activity in a sample, and for modulating telomere
 CC length in a cell.
 XX
 SQ Sequence 1166 AA;

Query Match 14.6%; Score 247.5; DB 21; Length 1166;
 Best Local Similarity 23.4%; Pred. No. 5.3e-15;
 Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;
 QY 24 NEKLGRDTRQKLPMDLLVLEDEKHGAQSAALQKVGQERVRKTS---LDLREIIDVG 79
 DB 408 sekahnd-----vvevvvkheakvnaIdnl-gqtslhraaycghlqtrlllsyg 456
 QY 80 GIONLIELR-----KKRQKKRDALA-ASHEPPPEPEEITGPVDEETFLK----- 123
 DB 457 cdnliislgftalqmgnenvvqllqegislgenseadrqlleaakagdvctvklctvgs 516
 QY 124 -----AAVEGKMVKIEKFLADGGADTCDFRFTALHRASLEGHMEILE 167
 DB 517 vncrdiegrqstplhfaagynrvsvveyllqhgadvhakdkgglvplhnacsyghyevae 576
 QY 209 TNVRDKLL-----SPLHVAVRTGQVEIVE 233
 DB 637 tdiqdlirgdaalldaakkgclarvkklsdpdncrdtqgrhstplhlaagynnlvae 596
 QY 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
 DB 697 yllqhgadvnaqdkgglliplhnaasyghvdaallikynacvnatdkwaftplheaakg 756
 QY 261 RYKIILKLLHGDMMTKNLAKGTPTDLVOLWQADTRHAL-----EHPE--- 304
 DB 757 rtqicalllhaagadtlnkdegtdpldlv---saddvsalltaampspalpsckypqvin 813
 QY 305 ----PGAENHGLEPNDSGRETPOQVPA 328
 DB 814 gvrspgataadal-----ssgspsspslsa 837

RESULT 15
 AAB66295
 D AAB66295 standard; Protein; 1166 AA.
 AC AAB66295;

XX 05-APR-2001 (first entry)
 XX Human tankyrase2 TANK2-SHORT SEQ ID NO: 135.
 XX Human; tankyrase2; TANK2; TRF1; telomere; cancer; neoplasm; aging;
 KW inflammatory disorder.
 XX Homo sapiens.
 OS
 XX WO200100849-A1.
 PN
 XX 04-JAN-2001.
 PD
 XX 28-JUN-2000; 2000WO-US17827.
 PF
 XX 29-JUN-1999; 99US-0141582.
 PR

XX (ICOS-) ICOS CORP.

XX Christenson E, Demaggio AJ, Goldman PS, McElligott DL;
 XX WPI; 2001-102896/11.
 XX N-PSDB; AAF63953.

XX New tankyrase2 polypeptides, useful for treating conditions mediated by
 PT poly(adenosine diphosphate-ribose) polymerase activity e.g. cancers,
 PT inflammatory and autoimmune disorders

XX Claim 3; Page 200-203; 242pp; English.

XX The present invention provides the protein and coding sequence for the
 CC human tankyrase2 protein. This is found in two different versions,
 CC designated TANK2-LONG and TANK2-SHORT. Tankyrase2 has
 CC polyADP-ribosylation activity and is involved in the modification of
 CC TRF1, which is a telomere-specific binding protein. The regulation of
 CC telomere length, in which TRF1 has a role, is linked to ageing and
 CC cancer. The sequences are useful in the treatment of cancers and
 CC inflammatory disorders.

XX Sequence 1166 AA;

Query Match 14.6%; Score 247.5; DB 22; Length 1166;
 Best Local Similarity 23.4%; Pred. No. 5.3e-15;
 Matches 105; Conservative 49; Mismatches 133; Indels 161; Gaps 13;

QY 24 NEKLGRDTRQKLPMDLLVLEDEKHGAQSAALQKVGQERVRKTS---LDLREIIDVG 79
 DB 408 sekahnd-----vvevvvkheakvnaIdnl-gqtslhraaycghlqtrlllsyg 456
 QY 80 GIONLIELR-----KKRQKKRDALA-ASHEPPPEPEEITGPVDEETFLK----- 123
 DB 457 cdnliislgftalqmgnenvvqllqegislgenseadrqlleaakagdvctvklctvgs 516
 QY 124 -----AAVEGKMVKIEKFLADGGADTCDFRFTALHRASLEGHMEILE 167
 DB 517 vncrdiegrqstplhfaagynrvsvveyllqhgadvhakdkgglvplhnacsyghyevae 576
 QY 168 KLLDNGATVDFODRLDCTAMHWACRGHLEVVVKLLQSHGA-----D 208
 DB 577 llvkhgavnnvadlwktplheaakgyeicklllqhgadtlnkdegtdpldlvkdgd 636
 QY 209 TNVRDKLL-----SPLHVAVRTGQVEIVE 233
 DB 637 tdiqdlirgdaalldaakkgclarvkklsdpdncrdtqgrhstplhlaagynnlvae 696
 QY 234 HFLSLGLEINARDREG-----DTALHDAVRLN 260
 DB 697 yllqhgadvnaqdkgglliplhnaasyghvdaallikynacvnatdkwaftplheaakg 756
 QY 261 RYKIILKLLHGDMMTKNLAKGTPTDLVOLWQADTRHAL-----EHPE--- 304
 DB 757 rtqicalllhaagadtlnkdegtdpldlv---saddvsalltaampspalpsckypqvin 813
 QY 305 ----PGAENHGLEPNDSGRETPOQVPA 328
 DB 814 gvrspgataadal-----ssgspsspslsa 837

Search completed: April 17, 2002, 08:10:16
 Job time: 34 sec

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ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
C.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719
A:Accession: C86212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-543 <STO>
A:Cross-references: GB:AE005172; NID:98439897; PIDN:AAF75083.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

Query Match 14.6%; Score 247.5; DB 2; Length 543;
Best Local Similarity 29.1%; Pred. No. 1.4e-09;
Matches 102; Conservative 48; Mismatches 121; Indels 79; Gaps 15;

QY 21 EEENEKLRGTRQKLP-----DLVLEDEKHHG-----AQAALQKVGK- 60
Db 2 EGEDTVAGSSIPKKMMKQLTGKRDITLHSAVRGKDRVVEILTITRESELNQLLGK 61
QY 61 QERVKTSIDLREITDVGION-----LIELRKKRKKRDAALASHEPPPEPEEI 112
Db 62 QNOSGETALVAAEYGDVEIVKEMINCYDIALVEI-----KARNGFDAFH----- 106
QY 113 TGPVDEETFLKAAVEGKMKVIEKFLADGGS--ADTCDFQFRRTALHRASLEGHMEILEKLL 170
Db 107 -----IAKQGDLDVL-KVLAESAHELAMTVDLSNTTALHTAATQGTVEVNFLL 155
QY 171 DNGATV-DFODRLDCTAMHWACRGHLEVVK-LLOSHGADTVNRKLLSTPLHVAVRTQ 228
Db 156 ELGSSLAGIAKNGKTALHSASRNGHVKIKALLASEPAITAIRMDKKGQTALHMAVKGYN 215
QY 229 VEIVEHFLSLG-LEINARDREGDTALHDVRLNRYKIIKLLILHG-ADMMTKNLAGKTP 286
Db 216 VEVVEELIKADRSINTADTKGNFTALHIAARKGFSQIVKLLANNTDITKAYNRSGT-- 273
QY 287 DLVOLWQADTRHAEHPE-----PGAENHGLEGNDSGRETPQPV 326
Db 274 -----ALDTAEKIGNPEVALILQKHGVPASAKTIKPSGNPA-RELKQTV 316

RESULT 3
T13940
ankyrin - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13940
Dubreuil, R.R.; Yu, J.
Proc. Natl. Acad. Sci. U.S.A. 91, 10285-10289, 1994
A>Title: Ankyrin and beta-spectrin accumulate independently of alpha-spectrin in Drosoph
A:Reference number: Z17820; MUID:95024098
A:Accession: T13940
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1549 <DUB>
A:Cross-references: EMBL:LJ5601; NID:9557083; PID:9557084; PIDN:AAAC37208.1
C:Genetics:
A:Cross-references: FlyBase:FBgn0011747

Query Match 14.1%; Score 238.5; DB 2; Length 1549;
Best Local Similarity 25.0%; Pred. No. 2.2e-08;
Matches 80; Conservative 51; Mismatches 120; Indels 69; Gaps 6;

QY 18 LAQEENEKLV-----RGDRQKLPMDLLVLEDEKHHGAQAALQKVGQERVKTSIDLRR 74
Db 451 LLOHEASADLPTIRGET-----PLHAAANQADIIRILLRSKVDIAIVREGQTPHVASR 506

QY 75 IDVGIGIQLIELRKKRKKOKKRDALAAASHEPPPEPEITGPVDEETFLKAAVEGKMKVIE 134
Db 507 LGNINIIMLLQHGCAINAQSNKYSALH-----IAAKEGQENIVQ 547
QY 135 KFLADGGSADTCDFQFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLDCT----- 185
Db 548 VLEENGAENNAVTKGFTPLHLACKYGNVVOILLONGASIDFGKNKDVTPLHVATHYN 507
QY 186 -----AMHWACRGHLEVVKLLQSHGADTVNRKLLSTPLH 221
Db 608 NPSTIVELLKNGSPNLCARNGQCAIHIACKKNYLSIAMQLLOHGADVNIISKGSFPLH 667
QY 222 VAVRTGOVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLILHGADMMTKNLA 281
Db 668 LAAQGGNVDMVQLLEYGV-ISAANKGLTPLHVAQAQEGHVLVSQILLHEGANISERTRN 726
QY 282 GKTP-----TDLVQLW 292
Db 727 GYTPLHMAAHYGHLDLVKFF 746

RESULT 4
D84448
probable ankyrin [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84448
R.; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
cuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: D84448
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-247 <STO>
A:Cross-references: GB:AE002093; NID:94335756; PIDN:AAD17433.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g03430
A:Map position: 2

Query Match 14.0%; Score 237.5; DB 2; Length 247;
Best Local Similarity 34.1%; Pred. No. 2.6e-09;
Matches 61; Conservative 32; Mismatches 75; Indels 11; Gaps 2;

QY 117 DEETFLKAAVEGKMKVIEKFLADGGSADTC-----DQFRRTALHRASLEGHMEILEKLLDN 172
Db 46 DGRSLHVAASFHSGHSQIVKLLSSDEAKTVINSKDEGWAPLHSAASIGNAELVEVLLTR 105
QY 173 GATVDFQDRLDCTAMHWACRGHLEVVKLLQSHGADTVNRKLLSTPLHVAVRTGOVEIV 232
Db 106 GADVNAKNGNGRTALHYAASKGRLEIAQLLLTHGAKINITDKVGCTPLHRAASVGKLEVC 165
QY 233 EHFSLGLEINARDREGDTALHDV-----RLNRYKIIKLLILHGADMMTKNLAGKT 284
Db 166 EFLIEEGAEIDATDKMGQTALMHSVICDDKQLKVMQDQVAFLLIRHGADVDEDEKGYT 224

RESULT 5
T43458
hypothetical protein DKF2p34F0621.1 - human
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T43458
R.; Blum, H.; Bauersachs, S.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z22517
A:Accession: T43458
A:Status: preliminary
A:Molecule type: mRNA

Matches 60; Conservative 29; Mismatches 87; Indels 3; Gaps 2;

QY 108 EPEITGPVDEETFLKAAVEGKMKVIEKFLADGGADTCDFRR-TALHRASLEGHMEIL 166
 Db 330 EIDDIT--LDHLTPLHVAACGHHVRVAKVLLDKGAKPNSRALNGFTPLHIAACKNHHVRVM 387
 QY 167 EKLIDNGATVDFQDLCTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
 Db 388 ELLKGTGASIDAVTESGLTPLHVAASFVGMHLPIVKNLQRGASPNVSNVKVETPLHMAARA 447
 QY 227 GQVEIVEHFLSLGLEINARDREGDTALHDVAVLNRYKIIKLLHGGADMTKNLAGKTP 285
 Db 448 GHTEVAKYLLQNKAKVNAKAKDDQTPHCAARIGHTNNVKKLLENNANPNLATTAGTTP 506

RESULT 8

SJHUK

N:Alternate names: ankyrin 2.1, erythrocyte; ankyrin-R

N:Contains: ankyrin 2.2

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999

C:Accession: S08275; A33219; PC2220; A35443

R:Lux, S.E.; John, K.M.; Bennett, V.

Nature 344, 36-42, 1990

#Title: Analysis of cDNA for human erythrocyte ankyrin indicates a repeated structure w

A:Reference number: S08275; MUID:90158830

A:Accession: S08275

A:Molecule type: mRNA

A:Residues: 1-1881 <LUX>

A:Cross-references: EMBL:X16609; NID:g28701; PIDN:CRA34610.1; PID:g28702

A:Accession: A33219

A:Molecule type: protein

A:Residues: 2-7, 'X', 9-17, 'X', 19-20, 'T', 22-30, 733-749, 'A', 751-753, 828-833, 'X', 835-855, 'X'

A:Note: 845-Arg and 1392-Thr were also found

R:Hermann, J.; Barel, M.; Frade, R.

Biochem. Biophys. Res. Commun. 204, 453-460, 1994

A:Title: Human erythrocyte ankyrin, a cytoskeleton component, generates the p57 membrane

A:Reference number: PC2220; MUID:95071348

A:Accession: PC2220

A:Molecule type: protein

A:Residues: 910-929 <HER>

R:David, L.H.; Bennett, V.

J. Biol. Chem. 265, 10589-10596, 1990

A:Title: Mapping the binding sites of human erythrocyte ankyrin for the anion exchanger

A:Reference number: A35443; MUID:90285190

A:Accession: A35443

A:Molecule type: protein

A:Residues: 'X', 5, 'X', 7-12, 403-417, 'X', 419-422, 'H', 424, 'LQ', 797-800, 'L', 802-814, 862-863,

C:Genetics:

A:Gene: GDB:ANK1; ANK

A:Cross-references: GDB:118737; OMIM:182900

#Map position: 8p11.2-8p11.2

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing; phosphoprotein

F:2-1881/Product: ankyrin 1, erythrocyte form 1 #status predicted <MAT1>

F:2-1512,1675-1881/Product: ankyrin 2.2, erythrocyte #status predicted <MAT2>

F:2-827/Domain: 89K #status predicted <DOM1>

F:2-827/Region: anion exchange protein binding

F:44-76/Domain: ankyrin repeat homology <AN01>

F:77-109/Domain: ankyrin repeat homology <AN02>

F:110-142/Domain: ankyrin repeat homology <AN03>

F:143-171/Domain: ankyrin repeat homology <AN04>

F:172-204/Domain: ankyrin repeat homology <AN05>

F:205-237/Domain: ankyrin repeat homology <AN06>

F:238-270/Domain: ankyrin repeat homology <AN07>

F:271-303/Domain: ankyrin repeat homology <AN08>

F:304-336/Domain: ankyrin repeat homology <AN09>

F:337-369/Domain: ankyrin repeat homology <AN10>

F:370-402/Domain: ankyrin repeat homology <AN11>

F:403-435/Domain: ankyrin repeat homology <AN12>

F:436-468/Domain: ankyrin repeat homology <AN13>

F:469-501/Domain: ankyrin repeat homology <AN14>
 F:502-534/Domain: ankyrin repeat homology <AN15>
 F:535-567/Domain: ankyrin repeat homology <AN16>
 F:568-600/Domain: ankyrin repeat homology <AN17>
 F:601-633/Domain: ankyrin repeat homology <AN18>
 F:634-666/Domain: ankyrin repeat homology <AN19>
 F:667-699/Domain: ankyrin repeat homology <AN20>
 F:700-732/Domain: ankyrin repeat homology <AN21>
 F:733-765/Domain: ankyrin repeat homology <AN22>
 F:766-798/Domain: ankyrin repeat homology <AN23>
 F:828-1382/Domain: 62K #status predicted <DOM2>
 F:828-1382/Region: spectrin binding
 F:1383-1881/Domain: 55K #status predicted <DOM3>

Query Match 13.9%; Score 234.5; DB 1; Length 1881;

Best Local Similarity 33.5%; Pred. No. 5.2e-08;

Matches 60; Conservative 29; Mismatches 87; Indels 3; Gaps 2;

QY 108 EPEITGPVDEETFLKAAVEGKMKVIEKFLADGGADTCDFRR-TALHRASLEGHMEIL 166
 Db 330 EIDDIT--LDHLTPLHVAACGHHVRVAKVLLDKGAKPNSRALNGFTPLHIAACKNHHVRVM 387
 QY 167 EKLIDNGATVDFQDLCTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
 Db 388 ELLKGTGASIDAVTESGLTPLHVAASFVGMHLPIVKNLQRGASPNVSNVKVETPLHMAARA 447
 QY 227 GQVEIVEHFLSLGLEINARDREGDTALHDVAVLNRYKIIKLLHGGADMTKNLAGKTP 285
 Db 448 GHTEVAKYLLQNKAKVNAKAKDDQTPHCAARIGHTNNVKKLLENNANPNLATTAGTTP 506

RESULT 9

S37431

N:Alternate names: ankyrin 2, neuronal long splice form - human

N:Contains: ankyrin 2, short form

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 13-Aug-1999

C:Accession: S37431; A39643; B39643; A40334; A49462; S14569

R:Chan, W.

Submitted to the EMBL Data Library, September 1993

A:Reference number: S37431

A:Accession: S37431

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-3924 <CHA>

A:Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288

R:Otto, E.; Kunimoto, M.; McLaughlin, T.; Bennett, V.

J. Cell Biol. 114, 241-253, 1991

A:Title: Isolation and characterization of cDNAs encoding human brain ankyrins reveal

A:Reference number: A39643; MUID:91302466

A:Accession: A39643

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-2077 <OT1>

A:Cross-references: GB:X56957

A:Accession: B39643

A>Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-1443,3585-3924 <OPT>

A:Cross-references: EMBL:X56958

R:Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux, S.E.; Wa

Genomics 10, 858-866, 1991

A:Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin gene.

A:Reference number: A40334; MUID:92009921

A:Accession: A40334

A:Molecule type: DNA

A:Residues: 463-474, 'PE', 477-495 <TSE>

A:Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648

R:Chan, W.; Kordeli, E.; Bennett, V.

J. Cell Biol. 123, 1463-1473, 1993

A:Title: 440-kD ankyrinB: structure of the major developmentally regulated domain and

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A;Residues: 1-1848 <BIR>  
A,Cross-references: EMBL:X69063; NID:g3l1816; PIDN:CAA48801.1; PTD:g3l1817  
C;Superfamily: ankynrin; ankynrin repeat homology  
C;Keywords: alternative splicing  
F;48-80/Domain: ankynrin repeat homology <AN01>  
F;81-113/Domain: ankynrin repeat homology <AN02>  
F;114-146/Domain: ankynrin repeat homology <AN03>  
F;147-175/Domain: ankynrin repeat homology <AN04>  
F;176-208/Domain: ankynrin repeat homology <AN05>  
F;209-241/Domain: ankynrin repeat homology <AN06>  
F;242-274/Domain: ankynrin repeat homology <AN07>  
F;275-307/Domain: ankynrin repeat homology <AN08>  
F;308-340/Domain: ankynrin repeat homology <AN09>  
F;341-373/Domain: ankynrin repeat homology <AN10>  
F;374-406/Domain: ankynrin repeat homology <AN11>  
F;407-439/Domain: ankynrin repeat homology <AN12>  
F;440-472/Domain: ankynrin repeat homology <AN13>  
F;473-505/Domain: ankynrin repeat homology <AN14>  
F;506-538/Domain: ankynrin repeat homology <AN15>  
F;539-571/Domain: ankynrin repeat homology <AN16>  
F;572-604/Domain: ankynrin repeat homology <AN17>  
F;605-637/Domain: ankynrin repeat homology <AN18>  
F;638-670/Domain: ankynrin repeat homology <AN19>  
F;671-703/Domain: ankynrin repeat homology <AN20>  
F;704-736/Domain: ankynrin repeat homology <AN21>  
F;737-769/Domain: ankynrin repeat homology <AN22>  
F;770-802/Domain: ankynrin repeat homology <AN23>
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	Query Match	13.8%	Score 233.5;	DB 2;	Length 1848;
BEST Local Similarity	34.1%;	Pred.	No. 6e+08;		
MATCHES	61;	Conservative	27;	Mismatches 88;	Indels 3; Gaps 2;

QY	108	EPEITGPVDEETFLKAAVEGKMVKIENFLADGGSNATCDQFRR-TALHRASLEGHWEIL	166
I : :: :	:	: :	:
IDBIT--LDHLTPLVHAACGHHRVAKVLLDKGAKPNSRALNGFTPLACKKNHIRVM	391		

Db 392 ELLLTKTASIDAVTVESGUTPLTVASFVSMGHPLPVKNLLQRGASPNVSNVKVETPLHHAARA 451
Qy 227 GQVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIILKLLLLHGADMMTKNLAKGTP 285
Db 452 GHTEVAKYLLQNKAKANAKAKDDQTPFHCAARIGHTGMVKLLLENGASPNLATTAGTTP 510

RESULT 11
I49502
ankyrin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C:Accession: I49502
R:White, R.A.; Birkenmeier, C.S.; Peters, L.L.; Barker, J.E.; Lux, S.E.
Mamm. Genome 3, 281-285, 1992
A:Title: Murine erythrocyte ankyrin cDNA: Highly conserved regions of the regulatory
A:Reference number: I49502; MUID:92345717
A:Accession: I49502
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1862 <RES>
A:Cross-references: GB:M84756; NID:g191939; PIDN:AAA37236.1; PID:g191940
C:Genetics:
A:Gene: Ank-1
C:Superfamily: ankyrin; ankyrin repeat homology
C:Keywords: alternative splicing
F:40-72/Domain: ankyrin repeat homology <AN01>
F:73-105/Domain: ankyrin repeat homology <AN02>
F:106-138/Domain: ankyrin repeat homology <AN03>
F:139-167/Domain: ankyrin repeat homology <AN04>
F:168-200/Domain: ankyrin repeat homology <AN05>
F:201-233/Domain: ankyrin repeat homology <AN06>
F:234-266/Domain: ankyrin repeat homology <AN07>
F:267-299/Domain: ankyrin repeat homology <AN08>

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000
C:Accession: T42713

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.
J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene
the repeat domain.

A:Reference number: Z22237; MUID:95340633

A:Accession: T42713

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1943 <PET>

A:Cross-references: EMBL:LA0632; NID:g710548; PID:g710550; PIDN:AAB01606.1

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

A:Introns: 855/1

C:Function:

A:Description: supposed to play an important role in the polarized distribution of many

A:Note: major kidney ankyrin

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 13.6%; Score 230; DB 2; Length 1943;
Best Local Similarity 25.9%; Pred. No. 1.1e-07;
Matches 78; Conservative 41; Mismatches 124; Indels 58; Gaps .7;

QY 22 ENEKLRGDTROKL-PMDLLVLEDEKHHGAQSAALQKVKGOERVKTSIDLRLREIID--- 77

Db -272 DRGAKIDAKTRDGLTPL-----HCGARS-----GHEQVVEMLDRSAPILSKTK 315

QY 78 -----YGGIQLNLIELRKKRQKRRDALAASH-----EPP 106

Db 316 NGLSPLHMATQGDHLNCVQLLQHNVPVDDVTNDVLTALHVAACHGHYKAVKVLDDKKAS 375

QY 107 PEPEITG--PVDEETFLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHME 164

Db 376 PNAKALNGFTPLH-----IACKKNRIRVMELLLKHGASTQAVTESGLTPIHVAAPFMGHVN 430

QY 165 ILEKLLDNGATVDFDRDLCTAMHWACRGHLEVVKLQSHGADTNVRDKLLSTPLHVAV 224

Db 431 IVSOLMHHGASPTNVRGETALHMAARSGQAEVRYLVQDGAQVEAKAKDDQTPHISA 490

QY 225 RTGQVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLHLHGADMMTKNLAKGT 284

Db 491 RLKGADIVQQLLQOGASPNAAATTSVYTPHLAAREGHEDVAAFLLDHGASLSITTKKGFT 550

QY 285 P 285

Db 551 P 551

RESULT 15

T42716

ankyrin 3, splice form 4 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 04-Mar-2000

C:Accession: T42716

R:Peterson, L.L.; John, K.M.; Lu, F.M.; Eicher, E.M.; Higgins, A.; Yialamas, M.; Turtzo, I.

J. Cell Biol. 130, 313-330, 1995

A:Title: Ank3 (epithelial ankyrin), a widely distributed new member of the ankyrin gene

the repeat domain.

A:Reference number: Z22237; MUID:95340633

A:Accession: T42716

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-1961 <PET>

A:Cross-references: EMBL:LA0632; NID:g710548; PID:g710552; PIDN:AAB01607.1

A:Experimental source: strain C57BL/6J; kidney

C:Genetics:

A:Gene: Ank3

A:Map position: 10

C:Superfamily: ankyrin; ankyrin repeat homology

C:Keywords: alternative splicing

Query Match 13.6%; Score 230; DB 2; Length 1961;

Best Local Similarity 25.9%; Pred. No. 1.1e-07;

Matches 78; Conservative 41; Mismatches 124; Indels 58; Gaps 7;

QY 22 ENEKLRGDTROKL-PMDLLVLEDEKHHGAQSAALQKVKGOERVKTSIDLRLREIID--- 77

Db 272 DRGAKIDAKTRDGLTPL-----HCGARS-----GHEQVVEMLDRSAPILSKTK 315

QY 78 -----YGGIQLNLIELRKKRQKRRDALAASH-----EPP 106

Db 316 NGLSPLHMATQGDHLNCVQLLQHNVPVDDVTNDVLTALHVAACHGHYKAVKVLDDKKAS 375

QY 107 PEPEITG--PVDEETFLKAAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHME 164

Db 376 PNAKALNGFTPLH-----IACKKNRIRVMELLLKHGASTQAVTESGLTPIHVAAPFMGHVN 430

QY 165 ILEKLLDNGATVDFDRDLCTAMHWACRGHLEVVKLQSHGADTNVRDKLLSTPLHVAV 224

Db 431 IVSOLMHHGASPTNVRGETALHMAARSGQAEVRYLVQDGAQVEAKAKDDQTPHISA 490

QY 225 RTGQVEIVEHFLSLGLEINARDREGDTALHDVRLNRYKIIKLLHLHGADMMTKNLAKGT 284

Db 491 RLKGADIVQQLLQOGASPNAAATTSVYTPHLAAREGHEDVAAFLLDHGASLSITTKKGFT 550

QY 285 P 285

Db 551 P 551

Search completed: April 17, 2002, 08:11:00

Job time: 78 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:10:22 ; Search time 13.29 Seconds
(without alignments)
907.654 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
Sequence: 1 MEDSEAVQATALLIEORLAQ.....NGLGNDSGRETPQVPQAQ 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum first 100%
Listing first 45 summaries

Database : SwissProt_39:*

* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	284.5	16.8	1059	1 Y379_HUMAN	O15084 homo sapien
2	245	14.5	692	1 Y957_HUMAN	Q9Y294 homo sapien
3	234.5	13.9	1880	1 ANK1_HUMAN	P16157 homo sapien
4	234.5	13.9	3924	1 ANK2_HUMAN	Q01484 homo sapien
5	233.5	13.8	1862	1 ANK1_MOUSE	Q02357 mus musculu
6	228.5	13.5	318	1 IKBA_CHICK	Q91974 gallus gall
7	224.5	13.3	768	1 YB23_HUMAN	Q9ULJ7 homo sapien
8	224	13.2	679	1 YB23_MOUSE	Q05921 mus musculu
9	217	12.8	741	1 RN5A_HUMAN	Q05823 homo sapien
10	215	12.7	323	1 ANKH_CHRVI	Q06527 chromatium
11	212	12.5	656	1 FEM1_CAEEL	P17221 caenorhabdi
12	208.5	12.3	347	1 GABC_MOUSE	Q00421 mus musculu
13	208.5	12.3	382	1 GABB_MOUSE	Q00420 mus musculu
14	207.5	12.3	347	1 GABB_HUMAN	Q06545 homo sapien
15	207.5	12.3	383	1 GABB_HUMAN	Q06547 homo sapien
16	203.5	12.0	1431	1 DAPK_HUMAN	P53355 homo sapien
17	202	11.9	832	1 ANR3_HUMAN	P57078 homo sapien
18	200.5	11.8	1401	1 LATYA_LATMA	P23631 latrodectus
19	198	11.7	314	1 IKBA_RAT	Q63746 rattus norv
20	196	11.6	314	1 IKBA_PIG	Q08353 sus scrofa
21	189.5	11.2	439	1 AKR_ARATH	Q05753 arabidopsis
22	187.5	11.1	317	1 IKBA_HUMAN	P25963 homo sapien
23	187	11.0	765	1 BAR1_MOUSE	O70445 mus musculu
24	185	10.9	168	1 CDN6_HUMAN	P42773 homo sapien
25	181	10.7	768	1 BAR1_RAT	Q9GZB2 rattus norv
26	180.5	10.7	1083	1 YIL2 YEAST	P40480 saccharomyc
27	179.5	10.6	2703	1 NOTC DROME	P07207 drosophila
28	178.5	10.5	764	1 AKR1 YEAST	P39010 saccharomyc
29	178.5	10.5	971	1 KBF1_MOUSE	P25799 mus musculu
30	176.5	10.4	238	1 IKBA_MOUSE	Q9ZLE3 mus musculu
31	176.5	10.4	414	1 GABD_MOUSE	P81069 mus musculu
32	175.5	10.4	522	1 KBF1_RAT	Q63369 rattus norv
33	174	10.3	984	1 KBF1_CHICK	Q04861 gallus gall

ALIGNMENTS

RESULT 1	Y379_HUMAN	STANDARD;	PRT; 1059 AA.
ID	Y379_HUMAN		
AC	O15084;		
DT	20-AUG-2001 (Rel. 40, Created)		
DT	20-AUG-2001 (Rel. 40, Last sequence update)		
DT	20-AUG-2001 (Rel. 40, Last annotation update)		
DE	HYPOTHETICAL PROTEIN KIAA0379 (FRAGMENT).		
GN	KIAA0379.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCB_TaxID=9606;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RX	MEDLINE=97349984; PubMed=9205841;		
RA	Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N.,		
RA	Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;		
RT	"Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."		
RL	DNA Res. 4:141-150(1997).		
CC	-1- SIMILARITY: CONTAINS AT LEAST 27 ANK REPEATS.		
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).		
CC	EMBL; AB002377; BAA20833.2; -		
CC	HSSP; P42771; 1BI7.		
DR	InterPro: IPR002110; ANK.		
DR	Pfam: PF00023; ank; 28.		
DR	SMART; SM00248; ANK; 26.		
DR	PROSITE; PS50088; ANK_REPEAT; 24.		
DR	PROSITE; PS50297; ANK_REPEAT; 1.		
KW	Hypothetical protein; Repeat; ANK repeat.		
FT	NON_TER 1		
FT	REPEAT 46 75		ANK 1.
FT	REPEAT 79 108		ANK 2.
FT	REPEAT 112 141		ANK 3.
FT	REPEAT 145 174		ANK 4.
FT	REPEAT 178 207		ANK 5.
FT	REPEAT 211 240		ANK 6.
FT	REPEAT 244 273		ANK 7.
FT	REPEAT 277 307		ANK 8.
FT	REPEAT 311 340		ANK 9.
FT	REPEAT 344 373		ANK 10.
FT	REPEAT 377 406		ANK 11.
FT	REPEAT 410 439		ANK 12.
FT	REPEAT 443 472		ANK 13.
FT	REPEAT 476 506		ANK 14.

P52273 homo sapien
P20749 homo sapien
Q60772 mus musculu
O14593 homo sapien
Q09701 schizosacch
Q62422 mus musculu
Q95728 homo sapien
P77736 escherichia
Q92205 mus musculu
P98150 gallus gall
P19838 homo sapien
P31695 mus musculu

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FT REPEAT      510    540    ANK 15.
FT REPEAT      555    584    ANK 16.
FT REPEAT      588    617    ANK 17.
FT REPEAT      622    651    ANK 18.
FT REPEAT      658    687    ANK 19.
FT REPEAT      691    720    ANK 20.
FT REPEAT      724    753    ANK 21.
FT REPEAT      761    790    ANK 22.
FT REPEAT      793    823    ANK 23.
FT REPEAT      828    857    ANK 24.
FT REPEAT      861    891    ANK 25.
FT REPEAT      895    924    ANK 26.
FT REPEAT      931    960    ANK 27.
SQ SEQUENCE     1059 AA; 113465 MW; C1F55E6CFE494770 CRC64;

Query Match          16.8%; Score 284.5; DB 1; Length 1059;
Best Local Similarity 37.38; Pred. No. 3.5e-12;
Matches 66; Conservative 32; Mismatches 76; Indels 3; Gaps 1;

QY 124 AAVEGKMVKIEFLADGGSDTCDFRRTALHRASLEGHMEILEKLLDNGAIVDFQDRLD 183
   || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 AAANKAVCAEKALVPLLSNVNVSRRAGRTALHHAASFSGHGEMVKLLISRGANINAFDKD 179

QY 184 CTAMHWACRGHLEVVKLLOSHGADTNVRDKLLSTPLHVAVRVGOVEIHFVHLSGLGLEIN 243
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 RRARIHAAAYGHIEVVYKKLVSHGAETCKDKRSKSTPLHAAAASSGMTSVYKYLIDLGVDNN 239

QY 244 ARDEGTALTADVLRLRYKIIFKLHLHGADMNTKNLAGKTPTDLVOLWQADTRHAL 300
   : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 240 EPNAYGNTPLVACYNQDVVVNELIDCGAIVNQNEKGFTP---LHFAAAATHGAL 293

RESULT 2
Y957 HUMAN STANDARD; PRT; 692 AA.
ID Y957_HUMAN STANDARD; PRT; 692 AA.
AC Q9T2G4; O9NU24; O9UFO9;
DT -20-AUG-2001 (Rel. 40, Created)
DT -20-AUG-2001 (Rel. 40, Last sequence update)
DT -20-AUG-2001 (Rel. 40, Last annotation update)
DE HYPOTHETICAL PROTEIN KIAO0957.
OS Homo sapiens (Human).
GN Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Braint;
RX MEDLINE=99246063; PubMed=10231032;
SA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosewa M.,
SA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
SA "Prediction of the coding sequences of unidentified human genes. XIII.
RT The complete sequences of 100 new cDNA clones from brain which code
RL for large proteins in vitro.";
RL DNA Res. 6:63-70(1999).
RN [2]
RP SEQUENCE OF 67-692 FROM N.A. (ISOFORM 2).
RN [2]
RC TISSUE=Testis;
RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP SEQUENCE OF 140-692 FROM N.A. (ISOFORM 1).
RA Tracey A.;
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; MAY BE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 8 ANK REPEATS.
CC -----
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```

"cDNA sequence for human erythrocyte ankryrin.":
Proc. Natl. Acad. Sci. U.S.A. 87:1730-1734(1990).
[3]
VARIANT HS ILE-462.
MEDLINE=96225450; PubMed=8640229;
Eber S.W., Gonzalez J.M., Lux M.L., Scarpa A.L., Tse W.T.,
Dornwell M., Herbers J., Kugler W., Oezcan R., Pekrun A.,
Gallagher P.G., Schroeter W., Forget B.G., Lux S.E.,
"Ankyrin-1 mutations are a major cause of dominant and recessive
hereditary spherocytosis.",
Nat. Genet. 13:214-218(1996).
-1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2, TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
-1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
-1- ALTERNATIVE PRODUCTS: VARIOUS ISOFORMS OF ANKYRIN ARE PRODUCED BY
ALTERNATIVE SPLICING. THE SEQUENCE SHOWN IS THAT OF ANKYRIN
VARIANT 2.1.
-1- PTM: REGULATED BY PHOSPHORYLATION.
-1- PTM: ACYLATED BY PALMITIC ACID GROUP(S).
-1- DISEASE: DEFECTS IN ANK1 ARE THE CAUSE OF DOMINANT AND RECESSIVE
HEREDITARY SPHEROCYTOSIS (HS).
-1- SIMILARITY: CONTAINS 23 ANK REPEATS.
-1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

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EMBL; X16609; CAA34610.1; -;
EMBL; M28880; AAM51732.1; -;
PIR; S08275; SJHUK.
PIR; A35049; A35049.
HSP; Q00420; 1AMC.
MIM; 182900; -;
InterPro; IPR002110; ANK.
InterPro; IPR000488; Death.
InterPro; IPR000906; ZU5.
Pfam; PF00023; ank; 23.
Pfam; PF00531; death; 1.
Pfam; PF00791; ZU5; 1.
SMART; SM00248; ANK; 22.
SMART; SM00005; DEATH; 1.
SMART; SM00218; ZU5; 1.
PROSITE; PS50088; ANK_REPEAT; 20.
PROSITE; PS50297; ANK_REPEAT_REGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
Phosphorylation; Lipoprotein; Multigene family; Disease mutation;
Elliptocytosis; Polymorphism.
INIT_MET 0
DOMAIN 1 826 89 KDA DOMAIN (ANTON EXCHANGE PROTEIN
BINDING DOMAIN).
DOMAIN 827 1381 62 KDA DOMAIN (SPECTRIN BINDING
DOMAIN).
DOMAIN 1382 1880 55 KDA REGULATORY DOMAIN (REGULATES
THE BINDING OF ANKYRIN TO SPECTRIN
AND THE BAND 3 PROTEIN).
REPEAT 43 72 ANK 1.
REPEAT 76 105 ANK 2.
REPEAT 109 138 ANK 3.
REPEAT 142 171 ANK 4.
REPEAT 173 200 ANK 5.
REPEAT 204 233 ANK 6.

FT REPEAT	237	266	ANK 7.
FT REPEAT	270	299	ANK 8.
FT REPEAT	303	332	ANK 9.
FT REPEAT	336	365	ANK 10.
FT REPEAT	369	398	ANK 11.
FT REPEAT	402	431	ANK 12.
FT REPEAT	435	464	ANK 13.
FT REPEAT	468	497	ANK 14.
FT REPEAT	501	530	ANK 15.
FT REPEAT	534	563	ANK 16.
FT REPEAT	567	596	ANK 17.
FT REPEAT	600	629	ANK 18.
FT REPEAT	633	662	ANK 19.
FT REPEAT	666	695	ANK 20.
FT REPEAT	699	728	ANK 21.
FT REPEAT	732	761	ANK 22.
FT REPEAT	765	794	ANK 23.
FT DOMAIN	1402	1486	DEATH.
FT VARSPLIC	1512	1873	MISSING (IN ISOFORM 2.2).
FT VARSPLIC	1874	1874	H -> D (IN ISOFORM 2.2).
FT VARSPLIC	1849	1880	TVEGPLEDSELEVIDIDYFMKHSKDHSTPNP -> ELRGS
FT			GLQPLIEGRKGAQIVKRLRGRQ (IN A THIRD
FT			ISOFORM).
FT			R -> T.
FT	20	20	/FTID-VAR_000595.
FT	462	462	V -> I (IN HS).
FT	618	618	/FTID-VAR_000596.
FT	749	749	R -> H (IN BRUEGEN).
FT	844	844	/FTID-VAR_000597.
FT	1285	1285	V -> A.
FT	1391	1391	/FTID-VAR_000598.
FT	1591	1591	D -> E.
FT	1698	1698	/FTID-VAR_000599.
FT	229	229	E -> D.
FT	1545	1545	/FTID-VAR_000601.
FT	1880	1880	S -> T.
FT			/FTID-VAR_000600.
FT			D -> N (IN DUESSELDORF).
FT			R -> D.
FT			/FTID-VAR_000603.
FT			A -> S (IN REF. 2).
FT			V -> I (IN REF. 2).
FT			SEQUENCE
FT			1C5F5E7EFD1CD428 CRC64;

Query Match 13.9%; Score 234.5; DB 1; Length 1880;
Best Local Similarity 33.5%; Pred. No. 2e-08;
Matches 60; Conservative 29; Mismatches 87; Indels 3; Gaps 2;
Qy 108 EPEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDFRR-TALHRASLEGHEIL 166
Db 329 EIDDT--LDHLTPLHVAACGHHVAKVLLDKGAKPNSRALNGFTPLHIAACKNHRVM 386
Qy 167 EKLLDNGATVDFQDLCTAMHWACRGHLEVVKLLSHGADTNVRKLLSTPLHVAVRT 226
Db 387 ELLLTGASIDAVTESGUTPLHVSFAGHLPIVKNLQRGASPNVSVKVTPLHMAARA 446
Qy 227 GQVEIVEHFLSLGLEINARDREGDTALHDAVRLNRYKIILKLLHGLGADMTKNLGKTP 285
Db 447 GHTEVAKYLLQNKAKVNAKAKDDQPLHCAARIGHTNNVKKLLENANPNLATAGHTP 505
RESULT 4
ID ANK2_HUMAN STANDARD; PRT; 3924 AA.
AC Q01484; Q01485;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANKYRIN 2 (BRAIN ANKYRIN) (ANKYRIN B) (ANKYRIN, NONERYTHROID).
GN ANK2.
OS Homo sapiens (Human).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain stem;
RX MEDLINE=94075409; PubMed=8253844;
RA Chan W., Kordeli E., Bennett V.;
RT "440-kb ankyrinB: structure of the major developmentally regulated
domain and selective localization in unmyelinated axons.";
RL J. Cell Biol. 123:1463-1473(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RC TISSUE=Brain stem;
RX MEDLINE=91302466; PubMed=1830053;
RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;
RT "Isolation and characterization of cDNAs encoding human brain
ankyrins reveal a family of alternatively spliced genes.";
RL J. Cell Biol. 114:241-253(1991).
RN [3]
RP REVISIONS.
RA Carpenter S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 463-495 FROM N.A.
RX MEDLINE=92009921; PubMed=1833308;
RA Tse W.T., Menninger J.C., Tang-Feng T.L., Francke U., Sahr K.E.,
RL Lux S.E., Ward D.C., Forget B.G.;
RT "Isolation and chromosomal localization of a novel nonerythroid
ankyrin gene.";
RL Genomics 10:858-866(1991).
CC -1- FUNCTION: ANKYRINS ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTO-
SKELETAL ELEMENTS; THEY BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN
BAND 4.2, TO NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85,
AND TO THE CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND
DESMIN. ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO
THE CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE
PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: PLASMA MEMBRANE OF NEURONS AS WELL AS GLIAL
CELLS THROUGHOUT THE BRAIN.
CC -1- PTM: PHOSPHORYLATED AT MULTIPLE SITES BY DIFFERENT PROTEIN KINASES
AND EACH PHOSPHORYLATION EVENT REGULATES THE PROTEIN'S STRUCTURE
AND FUNCTION (POTENTIAL).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL; Z26634; CAB42644.1; -
DR EMBL; X56957; CAA40278.1; -
DR EMBL; X56958; CAA40279.2; -
DR EMBL; M37123; AAA62828.1; -
DR PIR; S14533; S14533.
DR PIR; A39643; A39643.
DR PIR; B39643; B39643.
DR PIR; S14569; S14569.
DR HSP; Q00420; IAWC.
DR MIM; 106410; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000906; ZU5.
DR Pfam; PF00023; ank; 24.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00791; ZU5; 1.
DR SMART; SM00248; ANK; 21.

DR SMART; SM00005; DEATH; 1.
DR SMART; SM00218; ZU5; 1.
DR PROSITE; PS50088; ANK_REPEAT; 20.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW Phosphorylation; Multigene family.
FT REPEAT 63 92 ANK 1.
FT REPEAT 96 125 ANK 2.
FT REPEAT 129 158 ANK 3.
FT REPEAT 162 191 ANK 4.
FT REPEAT 193 220 ANK 5.
FT REPEAT 232 261 ANK 6.
FT REPEAT 265 294 ANK 7.
FT REPEAT 298 327 ANK 8.
FT REPEAT 331 360 ANK 9.
FT REPEAT 364 393 ANK 10.
FT REPEAT 397 426 ANK 11.
FT REPEAT 430 459 ANK 12.
FT REPEAT 463 492 ANK 13.
FT REPEAT 496 525 ANK 14.
FT REPEAT 529 558 ANK 15.
FT REPEAT 562 591 ANK 16.
FT REPEAT 595 624 ANK 17.
FT REPEAT 628 657 ANK 18.
FT REPEAT 661 690 ANK 19.
FT REPEAT 694 723 ANK 20.
FT REPEAT 727 756 ANK 21.
FT REPEAT 760 789 ANK 22.
FT REPEAT 793 822 ANK 23.
FT REPEAT 825 854 REPEAT-RICH REGION.
FT REPEAT 857 886 REPEAT A.
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QY 297 -----RHLEHPEPGAEHNGLEPNDSGRET 322
Db 816 VTEEVTTTTTITEKHLNVPETWTE--VLDVSDDEGDDT 853

RESULT 5
ANK1_MOUSE STANDARD; PRT; 1862 AA.
ID ANK1_MOUSE
AC Q02357;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ANKYRIN 1 (ERYTHROCYTE ANKYRIN).
GN ANK1 OR ANK-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
RP TISSUE-Erythrocyte;
RC MEDLINE=92345717; PubMed=1386265;
RA White R.A., Birkenmeier C.S., Peters L.L., Barker J.E., Lux S.E.;
RT "Murine erythrocyte ankyrin cDNA: highly conserved regions of the
regulatory domain";
RL Mamm. Genome 3:281-285(1992).
CC -1- FUNCTION: ATTACH INTEGRAL MEMBRANE PROTEINS TO CYTOSKELETAL
ELEMENTS; BIND TO THE ERYTHROCYTE MEMBRANE PROTEIN BAND 4-2. TO
NA-K ATPASE, TO THE LYMPHOCYTE MEMBRANE PROTEIN GP85, AND TO THE
CYTOSKELETAL PROTEINS FODRIN, TUBULIN, VIMENTIN AND DESMIN.
CC ERYTHROCYTE ANKYRINS ALSO LINK SPECTRIN (BETA CHAIN) TO THE
CYTOPLASMIC DOMAIN OF THE ERYTHROCYTES ANION EXCHANGE PROTEIN;
CC THEY RETAIN MOST OR ALL OF THESE BINDING FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF ERYTHROCYTIC
PLASMA MEMBRANE.
CC -1- PTM: REGULATED BY PHOSPHORYLATION (BY SIMILARITY).
CC -1- PTM: ACYLATED BY PALMITIC ACID GROUP(S) (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 23 ANK REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M84756; AAA37236.1; -
CC HSSP; Q00420; 1ANC.
CC MGD; MGI:88024; Ank1.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR000488; Death.
CC Pfam; PF00023; ank; 24.
CC Pfam; PF00531; death; 1.
CC Pfam; PF00791; ZUS; 1.
CC SMART; SM00248; ANK; 22.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00218; ZUS; 1.
CC PROSITE; PS50088; ANK_REPEAT; 20.
CC PROSITE; PS50297; ANK_REPEAT_REGION; 1.
CC PROSITE; PS50017; DEATH_DOMAIN; 1.
CC Cytokeleton; Repeat; ANK repeat; Phosphorylation; Lipoprotein.
CC DOMAIN 1 827 89 KDA DOMAIN (ANION EXCHANGE PROTEIN
BINDING DOMAIN).
CC DOMAIN 828 1386 62 KDA DOMAIN (SPECTRIN BINDING
DOMAIN).
CC DOMAIN 1387 1862 55 KDA REGULATORY DOMAIN (REGULATES
THE BINDING OF ANKYRIN TO SPECTRIN
AND THE BAND 3 PROTEIN).
CC REPEAT 40 69 ANK 1.
CC REPEAT 73 102 ANK 2.

FT REPEAT 106 135 ANK 3.
FT REPEAT 139 168 ANK 4.
FT REPEAT 170 197 ANK 5.
FT REPEAT 201 230 ANK 6.
FT REPEAT 234 263 ANK 7.
FT REPEAT 267 296 ANK 8.
FT REPEAT 300 329 ANK 9.
FT REPEAT 333 362 ANK 10.
FT REPEAT 366 395 ANK 11.
FT REPEAT 399 428 ANK 12.
FT REPEAT 432 461 ANK 13.
FT REPEAT 465 494 ANK 14.
FT REPEAT 498 527 ANK 15.
FT REPEAT 531 560 ANK 16.
FT REPEAT 564 593 ANK 17.
FT REPEAT 597 626 ANK 18.
FT REPEAT 630 659 ANK 19.
FT REPEAT 663 692 ANK 20.
FT REPEAT 696 725 ANK 21.
FT REPEAT 729 758 ANK 22.
FT REPEAT 762 791 ANK 23.
FT DOMAIN 1399 1483 DEATH.
SQ SEQUENCE 1862 AA; 204242 MW; AEG6B85B5B29001E5 CRC64;

Query Match 13.8%; Score 233.5; DB 1; Length 1862;
Best Local Similarity 34.1%; Pred. No. 2.3e-08;
Matches 61; Conservative 27; Mismatches 88; Indels 3; Gaps 2;

QY 108 EPEETGPDVETELKAAVEGKMKVIEKFLADGSGADTCDFRR-TALHRSASLEHMEIL 166
Db 326 EIDDT--LDHLTPLHVAAGHGRVAKVLLDKGAKPNRSLNGFTPLHIAKKNHIRM 383
QY 167 EKLDNGATVDFQDRDCTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRT 226
Db 384 ELLKGTASIDAVTESGLTPLHVASFMGHLPIVKNLLQRGASPNVSNKVTPLHMAARA 443
QY 227 GQVEIVHFLSGLLEINARDREGDTALHDVRLNRYKIKILLHGGADMVTKNLAKTTP 285
Db 444 GHTEVAYKLLONKAKANAKAKDDQTLPCAARIGHTGMVKVLLLENGASPNLATTAGHTP 502

RESULT 6
IKBA_CHICK STANDARD; PRT; 318 AA.
ID IKBA_CHICK
AC Q91974;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE NF-KAPPAB INHIBITOR ALPHA (I-KAPPA-B-ALPHA) (IKAPPABALPHA) (IKB-ALPHA)
(REL-ASSOCIATED PROTEIN PP40).
GN NFKBIA OR IKBA.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryonic fibroblast;
RX MEDLINE=91368196; PubMed=1891714;
RA Davis N., Ghosh S., Simmons D.L., Tempst P., Liou H.-C., Baltimore D.,
RA Bose H.R. Jr.;
RT "Rel-associated pp40: an inhibitor of the rel family of transcription
factors";
RL Science 253:1268-1271(1991).
CC -1- FUNCTION: INHIBITOR OF NF-KAPPA-B THAT TIGHTLY REGULATES NF-KAPPA-
B ACTIVATION BY COMPLEXING AND TRAPPING IT IN THE CYTOPLASM. MAY
BE INVOLVED IN REGULATION OF TRANSCRIPTIONAL RESPONSES TO NF-
KAPPA-B, INCLUDING CELL ADHESION, IMMUNE AND PROINFLAMMATORY
RESPONSES, APOPTOSIS, DIFFERENTIATION AND GROWTH. CONTROLLED BY
SEQUENTIAL SERINE-PHOSPHORYLATION, UBIQUITINATION AND DEGRADATION.
CC TYROSINE-PHOSPHORYLATION COULD ONLY LEAD TO DISSOCIATION FROM NF-
CC

Db 352 RSALQSAAMQGHVKKVQLLIEHGAUVVHTCNOGATACALCTAAQEGHIDVVQVLLHGAADPN 411
 QY 244 ARDEGDTALHDAVRLNRKIILKLLHGCADMMTKNLAKGTPTDVLQVQWADTRALE 301
 Db 412 HADQFGRTAMRVAAKNGHSQIILKLEKYGA-----SSLNGCSPSPV-----HTME 456

RESULT 8
 ID RN5A_MOUSE STANDARD; PRT; 679 AA.
 AC Q05921;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNASE)
 DE (RIBONUCLEASE L) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).
 GN RNASEL OR RNS4.
 Mus musculus (Mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93201598; PubMed=7680958;
 RA Zhou A., Hassel B.A., Silverman R.H.;
 RT "Expression cloning of 2-5A-dependent RNase: a uniquely regulated
 mediator of interferon action."
 RL Cell 72:753-765(1993).
 CC -!- FUNCTION: MEDIATES THE EFFECTS OF INTERFERON AGAINST
 PICOINAVIRUSES. ACTIVE WHEN BOUND TO 2-5A (5'-PHOSPHORYLATED
 2',5'-LINKED OLIGONUCLEOTIDES). CAPABLE OF CLEAVING POLY(RU) AND,
 TO A LESSER EXTENT, POLY(RA), TO SETS OF DISCRETE PRODUCTS RANGING
 FROM BETWEEN 4 AND 22 NUCLEOTIDES IN LENGTH.
 CC -!- CATALYTIC ACTIVITY: CLEAVES 3' OF UPNP DIMERS, WITH PREFERENCE
 FOR UU AND UA SEQUENCES.
 CC -!- COFACTOR: OPTIMAL RNA CLEAVAGE RATES REQUIRES THE PRESENCE OF
 EITHER MANGANESE OR MAGNESIUM AND ATP.
 CC -!- SUBUNIT: MONOMER.
 CC -!- INDUCTION: BY INTERFERON.
 CC -!- SIMILARITY: CONTAINS 9 ANK REPEATS.
 CC -----
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 or send an email to license@isb-sib.ch.
 CC -----
 DR EMBL; L10382; AAA37117.1;
 DR HSSP; Q00420; 1AWC.
 DR MGD; MG1:1098272; Rnsel.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR007019; Euk_pkinase.
 DR Pfam; PF00023; ank; 8.
 DR Pfam; PF00069; pkinase; 1.
 DR SMART; SM00248; ANK; 7.
 DR PROSITE; PS50088; ANK_REPEAT; 7.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR Hydrolase; Nuclease; RNA-binding; Endonuclease; Zinc-finger;
 KW Repeat; ANK repeat.
 KW REPEAT 24 53 ANK 1.
 KW REPEAT 58 87 ANK 2.
 KW REPEAT 91 120 ANK 3.
 KW REPEAT 124 153 ANK 4.
 KW REPEAT 167 197 ANK 5.
 KW REPEAT 201 234 ANK 6.
 KW REPEAT 238 268 ANK 7.
 KW REPEAT 272 301 ANK 8.
 KW REPEAT 303 328 ANK 9.
 KW REPEAT 364 584
 FT DOMAIN 229
 FT 2-5A BINDING (P-LOOP) 1.

FT DOMAIN 253 275 2-5A BINDING (P-LOOP) 2.
 FT ZN_FING 401 436 C6-TYPE (POTENTIAL).
 FT NON_TER 679 679
 SQ SEQUENCE 679 AA; 76800 MW; 507DB36B62EC1F4D CRC64;
 Query Match 13.28; Score 224; DB 1; Length 679;
 Best Local Similarity 28.18; Pred. No. 2.9e-08;
 Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
 QY 41 VLEDEKHHGAOSAALOKVKGOERVRKTSLLDLRRLREITVDVGGIQLIE-----LRKKRKQ 93
 Db 22 VVEDD-----SSLIKAVQKGVVRV-----QQLLEKAGADANACEDTWGTPPLHNAVQA 69
 QY 94 KKRDA--LAAASHEPPEPEETPGVDETFLLKAAVEGKMKVIEKFLADGGSADTCQ--- 148
 Db 70 GRVDIVNLLSHGADPHRRKKNGAT---PFIAGIQGVKLLLEILLSCGADVNECDENG 126
 QY 149 -----FR-----TALHRASLEGHMEILEK 168
 Db 127 TAFMEAAERGNAAELRFLFAKGVNLRRTTKRRRLKQGGATALMSAAEKHLEVLRI 186
 QY 169 LL-DNGATVDFODR-----LDCTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHV 222
 Db 187 LLNDKMAEVDARDNMGRLIRTLNWDENVE-EITSILIQHGADVNVGRGKTPLIA 245
 QY 223 AVRTGOVEIVEHFLSL-GLEINARREGDTALHDVRLNRKIILKLLHGCADMMTKLA 281
 Db 246 AVERKHTGLVQMLLSREGINIDARDNEGTALLIAVDKQLKEIVQLLEKAGDKC----- 300
 QY 282 GKTPDVLQVQWADTRAH 298
 Db 301 ----DDLV--WIARNH 311
 RESULT 9
 ID RN5A_HUMAN STANDARD; PRT; 741 AA.
 AC Q05823;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DE 20-AUG-2001 (Rel. 40, Last annotation update)
 DE 2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DEPENDENT RNASE)
 DE (RIBONUCLEASE L) (RNASE L) (RIBONUCLEASE 4).
 GN RNASEL OR RNS4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=93201598; PubMed=7680958;
 RA Zhou A., Hassel B.A., Silverman R.H.;
 RT "Expression cloning of 2-5A-dependent RNase: a uniquely regulated
 mediator of interferon action."
 RL Cell 72:753-765(1993).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=94245737; PubMed=7514601;
 RA Dong B., Xu L., Zhou A., Hassel B.A., Lee X., Torrence P.F.,
 RA Silverman R.H.;
 RT "Intrinsic molecular activities of the interferon-induced 2-5A-
 dependent RNase."
 RL J. Biol. Chem. 269:14153-14158(1994).
 CC -!- FUNCTION: MEDIATES THE EFFECTS OF INTERFERON AGAINST
 PICOINAVIRUSES. ACTIVE WHEN BOUND TO 2-5A (5'-PHOSPHORYLATED
 2',5'-LINKED OLIGONUCLEOTIDES). CAPABLE OF CLEAVING POLY(RU) AND,
 TO A LESSER EXTENT, POLY(RA), TO SETS OF DISCRETE PRODUCTS RANGING
 FROM BETWEEN 4 AND 22 NUCLEOTIDES IN LENGTH.
 CC -!- CATALYTIC ACTIVITY: CLEAVES 3' OF UPNP DIMERS, WITH PREFERENCE
 FOR UU AND UA SEQUENCES.
 CC -!- COFACTOR: OPTIMAL RNA CLEAVAGE RATES REQUIRES THE PRESENCE OF

Matches 64; Conservative 34; Mismatches 101; Indels 31; Gaps 5;

QY 75 IIDVGGIQLNLELRKRKQKRDALAAASHPEPEPEITGPVDEETFLKAAVEGKMKVIE 134
Db 3 LVDLG--KKLEAARAGQDDEVIRLMANGAFPTDWTGTSPLH-----LAAQYGHFSTTE 55

QY 135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFODRLDCTAMHWACRG 194
Db 56 VLLRAGVSRDARTKVDRTPLHMAASEGHANIVEVLLKHGADVNAKMDLKMALHWATEHN 115

QY 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIHEHF--LSLGLLEINARDREGDTAL 253
Db 116 HQEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQIANQINPNESPDIT-- 173

QY 254 HDVAVLRNRYKIILKLLHGDMM-----TKNLAGTKPTDVLQWQADT 296
Db 174 -----VTIHAATPQFIIGPGVWNLTDETVSAVQFGNSST 209

RESULT 13

ID GABB_MOUSE STANDARD; PRT; 382 AA.

AC Q00420;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (GABPB1).

GN GABPB1 OR GABPB.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91343912; PubMed=1876836;

RA Lamarco K., Thompson C.C., Byers B.P., Walton E.M., McKnight S.L.;
RT "Identification of Ets- and notch-related subunits in GA binding
protein.";
RL Science 253:789-792(1991).

RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF 5-157.

RX MEDLINE=98128030; PubMed=9461436;

RA Batchelor A.H., Piper D.E., de la Brousse F.C., McKnight S.L.,
RA Wolberger C.;
RT "The structure of GABPalpha/beta: an ETS domain-ankyrin repeat
heterodimer bound to DNA.";
RL Science 279:1037-1041(1998).

CC -!- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE
RICH REPEATS (GA REPEATS).

CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.

CC -!- ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY
DIFFER IN THEIR C-TERMINAL EXTREMITY.

CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.

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CC EMBL; M74516; AAA53031.1; -

DR PIR; B40858; B40858.

DR PDB; 1AWC; 1B-MAR-98.

DR TRANSFAC; T00298; -

DR TRANSFAC; T01403; -

DR MGD; MGI:95611; Gabpb1.

DR InterPro; IPR002110; ANK.

DR Pfam; PF00023; ank; 3.

DR SMART; SM00248; ANK; 3.

DR PROSITE; PS50088; ANK_REPEAT; 3.

DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.

KW Transcription regulation; Nuclear protein; Alternative splicing;

FT ANK repeat; Repeat; 3D-structure.

FT REPEAT 5 34 ANK 1.

FT REPEAT 37 66 ANK 2.

FT REPEAT 70 99 ANK 3.

FT REPEAT 103 132 ANK 4.

FT REPEAT 136 166 ANK 5.

SQ SEQUENCE 382 AA; 41258 MW; 0A5FE3F71D4227AF CRC64;

Query Match 12.3%; Score 208.5; DB 1; Length 382;
Best Local Similarity 27.8%; Pred. No. 1.6e-07;
Matches 64; Conservative 34; Mismatches 101; Indels 31; Gaps 5;

QY 75 IIDVGGIQLNLELRKRKQKRDALAAASHPEPEPEITGPVDEETFLKAAVEGKMKVIE 134
Db 3 LVDLG--KKLEAARAGQDDEVIRLMANGAFPTDWTGTSPLH-----LAAQYGHFSTTE 55

QY 135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFODRLDCTAMHWACRG 194
Db 56 VLLRAGVSRDARTKVDRTPLHMAASEGHANIVEVLLKHGADVNAKMDLKMALHWATEHN 115

QY 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIHEHF--LSLGLLEINARDREGDTAL 253
Db 116 HQEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQIANQINPNESPDIT-- 173

QY 254 HDVAVLRNRYKIILKLLHGDMM-----TKNLAGTKPTDVLQWQADT 296
Db 174 -----VTIHAATPQFIIGPGVWNLTDETVSAVQFGNSST 209

RESULT 14

ID GABC_HUMAN STANDARD; PRT; 347 AA.

AC Q06545;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION
FACTOR E4TF1-47) (GABPB2).

GN GABPB1 OR GABPB OR E4TF1B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93180783; PubMed=8441384;

RA Watanabe H., Sawada J.-I., Yano K.-I., Yamaguchi K., Goto M.,
RA Handa H.;
RT "cDNA cloning of transcription factor E4TF1 subunits with Ets and
notch motifs";
RL Mol. Cell. Biol. 13:1395-1391(1993).

CC -!- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE
RICH REPEATS (GA REPEATS). NECESSARY FOR THE EXPRESSION OF THE
ADENOVIRUS E4 GENE.

CC -!- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.

CC -!- ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE
PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY
DIFFER IN THEIR C-TERMINAL EXTREMITY.

CC -!- SIMILARITY: CONTAINS 5 ANK REPEATS.

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CC EMBL; D13316; BAA02573.1; -

DR HSSP; Q00420; IAWC.

TRANSFAC; T01392; -
 MIN; 600610; -
 DR InterPro: IPR002110; ANK.
 DR Pfam; PF00023; ank; 3.
 DR SMART; SM00248; ANK; 3.
 DR PROSITE; PS00088; ANK_REPEAT; 3.
 DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 KW Transcription regulation; Nuclear protein; Alternative splicing;
 KW ANK repeat; Repeat.
 FT REPEAT 34 ANK 1.
 FT REPEAT 37 66 ANK 2.
 FT REPEAT 70 99 ANK 3.
 FT REPEAT 103 132 ANK 4.
 FT REPEAT 136 166 ANK 5.
 SQ SEQUENCE 347 AA; 36850 MW; 902C02A3F6ABBA2E CRC64;

Query Match 12.3%; Score 207.5; DB 1; Length 347;
 Best Local Similarity 27.8%; Pred. No. 1.7e-07;
 Matches 64; Conservative 34; Mismatches 101; Indels 31; Gaps 5;

Qy 75 IIDVGGIONLIELKRRKQKRDALAAASHEPPPEETPGVDETFLLKAAVEGKMKVIE 134
 Db 3 LVDLG--KKLLEAARAGQDDEVIRILMANGAPFTDWTGTSPLH-----LAAQYGHYSTTE 55

Qy 135 KFLADGGSADTCQDPRRTALHRASLEGHMEILEKLLDNGATVDFODRLDCTAMHWACRG 194
 Db 56 VLLRAGVSRDARTKVDRTPLHMAASEGHASIVEVLKKGADVNAKMDLKMALHWATEHN 115

Qy 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIYEHF-LSGLGLEINARDREGDTAL 253
 Db 116 HOEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQIAMQNTNPESPD-- 173

Qy 254 HDAVRLNRYKIILLHGGADM-----TKNLAGKPTDVLQWQADT 296
 Db 174 -----VTIHAATPQFIIGPGVVNLDTGVSNAVQFGNSST 209

RESULT 15
 ID GABP_HUMAN STANDARD; PRT; 383 AA.
 AC Q06547;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GA BINDING PROTEIN BETA-1 CHAIN (GABP-BETA-1 SUBUNIT) (TRANSCRIPTION
 DE FACTOR E4TF1-53) (GABPB1) (NUCLEAR RESPIRATORY FACTOR-2 SUBUNIT BETA
 DE 2)
 GN GABPB1 OR GABPB OR E4TF1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93180783; PubMed=8441384;
 RA Watanabe H., Sawada J.-I., Yano K.-I., Yamaguchi K., Goto M.,
 RA Handa H.;
 RT "cDNA cloning of transcription factor E4TF1 subunits with Ets and
 RT notch motifs";
 RL Mol. Cell. Biol. 13:1385-1391(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95097980; PubMed=7799916;
 RA Gagneja S., Virbasius J.V., Scarpulla R.C.;
 RT "Four structurally distinct, non-DNA-binding subunits of human
 RT nuclear respiratory factor 2 share a conserved transcriptional
 RT activation domain";
 RL Mol. Cell. Biol. 15:102-111(1995).
 CC -1- FUNCTION: TRANSCRIPTION FACTOR CAPABLE OF INTERACTING WITH PURINE
 CC RICH REPEATS (GA REPEATS). NECESSARY FOR THE EXPRESSION OF THE
 CC ADENOVIRUS E4 GENE.
 CC -1- SUBUNIT: HETEROTETRAMER OF TWO ALPHA AND TWO BETA SUBUNITS.

-1- ALTERNATIVE PRODUCTS: THE BETA-1 AND BETA-2 SUBUNITS ARE
 PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE AND ONLY
 DIFFER IN THEIR C-TERMINAL EXTREMITY.
 -1- SIMILARITY: CONTAINS 5 ANK REPEATS.

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 or send an email to license@sib-sib.ch).

EMBL; D13317; BAA02574.1; -
 EMBL; U13046; AAA65708.1; -
 HSP; Q00420; IAWC.
 TRANSFAC; T01391; -
 MIM; 600610; -
 InterPro; IPR002110; ANK.
 Pfam; PF00023; ank; 3.
 SMART; SM00248; ANK; 3.
 PROSITE; PS00088; ANK_REPEAT; 3.
 PROSITE; PS0297; ANK_REPEAT_REGION; 1.
 KW Transcription regulation; Nuclear protein; Alternative splicing;
 KW ANK repeat; Repeat.

FT REPEAT 5 34 ANK 1.
 FT REPEAT 37 66 ANK 2.
 FT REPEAT 70 99 ANK 3.
 FT REPEAT 103 132 ANK 4.
 FT REPEAT 136 166 ANK 5.
 SQ SEQUENCE 383 AA; 41321 MW; 07E7081A60016288 CRC64;

Query Match 12.3%; Score 207.5; DB 1; Length 383;
 Best Local Similarity 27.8%; Pred. No. 1.9e-07;
 Matches 64; Conservative 34; Mismatches 101; Indels 31; Gaps 5;

Qy 75 IIDVGGIONLIELKRRKQKRDALAAASHEPPPEETPGVDETFLLKAAVEGKMKVIE 134
 Db 3 LVDLG--KKLLEAARAGQDDEVIRILMANGAPFTDWTGTSPLH-----LAAQYGHYSTTE 55

Qy 135 KFLADGGSADTCQDPRRTALHRASLEGHMEILEKLLDNGATVDFODRLDCTAMHWACRG 194
 Db 56 VLLRAGVSRDARTKVDRTPLHMAASEGHASIVEVLKKGADVNAKMDLKMALHWATEHN 115

Qy 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIYEHF-LSGLGLEINARDREGDTAL 253
 Db 116 HOEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQIAMQNTNPESPD-- 173

Qy 254 HDAVRLNRYKIILLHGGADM-----TKNLAGKPTDVLQWQADT 296
 Db 174 -----VTIHAATPQFIIGPGVVNLDTGVSNAVQFGNSST 209

Search completed: April 17, 2002, 08:13:23
 Job time: 181 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: April 17, 2002, 08:09:42 ; Search time 12.56 Seconds
(without alignments)
589.457 Million cell updates/sec

Title: US-09-758-593A-1
Perfect score: 1693
Sequence: 1 MEDSAVQRATALIEQRLAQ.....NGLEGPNDSGRTPQVPQAQ 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

arched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A-COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B-COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A-COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B-COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS-COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	249.5	14.7	949	4	US-09-196-387-10
2	249.5	14.7	1327	4	US-09-196-387-2
3	234.5	13.9	1839	2	US-09-172-977-4
4	231.5	13.7	843	2	US-09-172-977-3
5	228	13.5	1088	4	US-09-082-059-2
6	224	13.2	679	2	US-08-462-481-4
7	224	13.2	679	2	US-08-436-771-6
8	224	13.2	679	2	US-08-434-998-6
9	224	13.2	679	2	US-08-487-797-6
10	224	13.2	679	2	US-08-701-005A-4
11	224	13.2	679	2	US-08-479-895-4
12	224	13.2	679	5	PCT-US95-02058-6
13	223	13.2	422	3	US-08-484-575A-6
14	223	13.2	422	3	US-08-477-459-6
15	223	13.2	422	3	US-08-479-869-6
16	223	13.2	422	4	US-08-486-414-6
17	223	13.2	422	5	PCT-US94-01826A-6
18	223	13.2	422	5	PCT-US94-02252A-6
19	219	12.9	679	3	US-08-943-956A-4
20	219	12.9	835	4	US-09-291-839-2
21	218.5	12.9	673	4	US-09-196-387-8
22	218.5	12.9	741	3	US-08-943-956A-2
23	217	12.8	741	2	US-08-462-481-2
24	217	12.8	741	2	US-08-436-771-2
25	217	12.8	741	2	US-08-436-771-4
26	217	12.8	741	2	US-08-434-998-2
27	217	12.8	741	2	US-08-434-998-4

28	217	12.8	741	2	US-08-487-797-2	Sequence 2, Appli
29	217	12.8	741	2	US-08-487-797-4	Sequence 4, Appli
30	217	12.8	741	2	US-08-701-005A-2	Sequence 2, Appli
31	217	12.8	741	2	US-08-479-895-2	Sequence 2, Appli
32	217	12.8	741	5	PCT-US95-02058-2	Sequence 2, Appli
33	217	12.8	741	5	PCT-US95-02058-4	Sequence 4, Appli
34	205.5	12.1	1745	2	US-09-031-485-33	Sequence 33, Appli
35	205.5	12.1	1745	2	US-08-847-429A-33	Sequence 33, Appli
36	205.5	12.1	1745	3	US-09-065-474-33	Sequence 33, Appli
37	203.5	12.0	1423	4	US-08-810-712-10	Sequence 10, Appli
38	202.5	12.0	314	2	US-08-989-478-3	Sequence 3, Appli
39	202.5	12.0	314	3	US-08-936-685-3	Sequence 3, Appli
40	201	11.9	352	3	US-09-065-474-139	Sequence 139, App
41	198	11.7	191	2	US-09-031-485-20	Sequence 20, Appli
42	198	11.7	191	2	US-08-847-429A-20	Sequence 20, Appli
43	198	11.7	191	3	US-09-065-474-20	Sequence 20, Appli
44	198	11.7	314	2	US-08-989-478-4	Sequence 4, Appli
45	198	11.7	314	3	US-08-936-685-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-196-387-10
; Sequence 10, Application US/09196387
; Patent No. 6277613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196.387
; FILING DATE: June 10, 1998
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 949 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-196-387-10

Query Match 14.7%; Score 249.5; DB 4; Length 949;
Best Local Similarity 26.2%; Pred. No. 3.4e-16;
Matches 91; Conservative 33; Mismatches 110; Indels 113; Gaps 9;

QY 40 LVLEDEKH---HGAQSAALQKVGOERVKTSLDLRRRIIDVGGION-----LIELR 88
 Db 484 LTYEFKGHSLQAAREADLAKV-----KT---LALIELNFKQPOSHETALHCAVASLH 534
 QY 89 KKRKO-----KKRDALAAASHPEPPPEETFGVDETFLLKAAVEGKMKVIE 134
 Db 535 PKRKQVTELLLRKGANVNEKNKDFMTPLH-----VAAERAHNDVME 575
 QY 135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNG-----173
 Db 576 VLHKGAKMNAIDTLGQTAALHRAALAGHLQTCRLLLSYGSDPSIISLOGFTAAQMGNEAV 635
 QY 174 -----ATVDFQ-----DRLDC-----TAMHWACRG 194
 Db 636 QQILSESTPIRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYN 695
 QY 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIYEHFSLGLEINARDREGDTALH 254
 Db 696 RVSVEYLLHHGADYHAKDKGLVPLHNACSYGHVEVAELLVRHGASVNVADLWKFTPLH 755
 QY 255 DAVRLNRYKIILKLLHGDMMTKNLAGTPTDVLQWQADTRHALE 301
 Db 756 EAAAKGYEICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLK 802

RESULT 2

US-09-196-387-2
 ; Sequence 2, Application US/09196387
 ; Patent No. 6277613
 ; GENERAL INFORMATION:
 ; APPLICANT: de Lange, Titia
 ; APPLICANT: Smith, Susan
 ; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
 ; TITLE OF INVENTION: OF USE THEREOF
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Klauber & Jackson
 ; STREET: 411 Hackensack Avenue, 4th Floor
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/196,387
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/095,225
 ; FILING DATE: June 10, 1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; TELEX: 133521
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1327 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; US-09-196-387-2

Query Match 14.7%; Score 249.5; DB 4; Length 1327;
 Best Local Similarity 26.2%; Pred. No. 5.6e-16;
 Matches 91; Conservative 33; Mismatches 110; Indels 113; Gaps 9;
 QY 40 LVLEDEKH---HGAQSAALQKVGOERVKTSLDLRRRIIDVGGION-----LIELR 88
 Db 484 LTYEFKGHSLQAAREADLAKV-----KT---LALIELNFKQPOSHETALHCAVASLH 534
 QY 89 KKRKO-----KKRDALAAASHPEPPPEETFGVDETFLLKAAVEGKMKVIE 134
 Db 535 PKRKQVTELLLRKGANVNEKNKDFMTPLH-----VAAERAHNDVME 575
 QY 135 KFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNG-----173
 Db 576 VLHKGAKMNAIDTLGQTAALHRAALAGHLQTCRLLLSYGSDPSIISLOGFTAAQMGNEAV 635
 QY 174 -----ATVDFQ-----DRLDC-----TAMHWACRG 194
 Db 636 QQILSESTPIRTSDVDYRLLEASKAGDLETVKQLCSSQNVNCRDLEGRHSTPLHFAAGYN 695
 QY 195 HLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIYEHFSLGLEINARDREGDTALH 254
 Db 696 RVSVEYLLHHGADYHAKDKGLVPLHNACSYGHVEVAELLVRHGASVNVADLWKFTPLH 755
 QY 255 DAVRLNRYKIILKLLHGDMMTKNLAGTPTDVLQWQADTRHALE 301
 Db 756 EAAAKGYEICKLLKHGADPTKKNRDGNTPLDLVKEGDTDIQDLK 802

RESULT 3

US-09-172-977-4
 ; Sequence 4, Application US/09172977
 ; Patent No. 5989863
 ; GENERAL INFORMATION:
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Yue, Henry
 ; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
 ; FILE REFERENCE: PF-0615 US
 ; CURRENT APPLICATION NUMBER: US/09/172,977
 ; CURRENT FILING DATE: 1998-10-14
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 4
 ; LENGTH: 1839
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE: -
 ; OTHER INFORMATION: g29491
 ; US-09-172-977-4
 Query Match 13.9%; Score 234.5; DB 2; Length 1839;
 Best Local Similarity 29.5%; Pred. No. 2.7e-14;
 Matches 65; Conservative 32; Mismatches 100; Indels 23; Gaps 3;
 QY 124 AAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQDRLD 183
 Db 636 RAAKNQMQIASTLLNNGAETNIVTKQVTPHLASQEGHTDMVTLDDKGANIHMSTKSG 695
 QY 184 CTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGQVEIYEHFSLGLEIN 243
 Db 696 LTSLLAAQEDKVNVDILTHGADQDAHTKLGYTFLIVACHYGNVKNVNFLLKQGANVN 755
 QY 244 ARDREGDTALHDAVRLNRYKIILKLLHGDMMTKNLAGTPTDVLQWQADTRHALE 296
 Db 756 AKTKNGYTPHQAQOAGGHTIINVLQHGAKPNATANGNTALAKRIGYISVVDTLKV 815
 QY 297 -----RHALEHPEPGAENHLEGPNDSGRET 322
 Db 816 VTVEVTTTTTTTTTEKHLNVPETMTE--VLDVSDEEGDDT 853

RESULT 4
US-09-172-977-3
; Sequence 3, Application US/09172977
; Patent No. 5989863
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
; FILE REFERENCE: PF-0615 US
; CURRENT APPLICATION NUMBER: US/09/172.977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 3
; LENGTH: 843
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE: -
; OTHER INFORMATION: g1841966
US-09-172-977-3

Query Match 13.7%; Score 231.5; DB 2; Length 843;
Best Local Similarity 29.1%; Pred. No. 1.8e-14;
Matches 64; Conservative 33; Mismatches 100; Indels 23; Gaps 3;
QY 124 AAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQDRILD 183
DB 601 AAKNMQIASTPLHNGAETNTVTKOGYTPPLHLSAQEGHDMVTLVLEKGANIHMSTKSG 660
QY 184 CTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFLSLGLEIN 243
DB 661 LTLHLAAEEDKVNADILTRHGADODAYTKLGYTPLIVACHYGNVKNVFLKOGANVN 720
QY 244 ARDREGDTALHDVRLNRYKIIKLLHGGADMTKNLAGKTPDLVQ-----LWQADT--- 296
DB 721 AKTKNGYTPLHQAQGGHTIINVLVHGAKPNATTANGNTALATKRLGIVSVVDTLKV 780
QY 297 -----RHLEHPEPGAHEHNGLEGNDSGRET 322
DB 781 VTEVTTTTTITEKHKLNAPEMTTE--VLVDSDEGDDT 818

RESULT 5
US-09-082-059-2
; Sequence 2, Application US/09082059A
; Patent No. 6225086
; GENERAL INFORMATION:
; APPLICANT: Moritow, Jon S.
; APPLICANT: Devarajan, Prasad
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identification
; FILE REFERENCE: 44574-5002-US
; CURRENT APPLICATION NUMBER: US/09/082.059A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/047356
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-082-059-2

Query Match 13.5%; Score 228; DB 4; Length 1088;
Best Local Similarity 33.3%; Pred. No. 5.7e-14;
Matches 54; Conservative 26; Mismatches 82; Indels 0; Gaps 0;
QY 124 AAVEGKMKVIEKFLADGGSADTCDFRRTALHRASLEGHMEILEKLLDNGATVDFQDRILD 183

DB 28 ACKNRIKVMELLKHGASIQAVTESGLTPIHVAAFMGHVNIVSOLMHHGASPNNTTVRG 87
QY 184 CTAMHWACRGHLEVVKLLQSHGADTNVRDKLLSTPLHVAVRTGOVEIVEHFLSLGLEIN 243
DB 88 ETALHMAARSQAQEVRYLVLDQGAQVEAKAKDDQPLHISARLGRADIVQQLQOGASPN 147
QY 244 ARDREGDTALHDVRLNRYKIIKLLHGGADMTKNLAGKTP 285
DB 148 AATTSGYTPLHLSAREGHEDVAAFLLDHGASLSITTKGFTP 189

RESULT 6
US-08-462-481-4
; Sequence 4, Application US/08462481
; Patent No. 5840577
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Almin
; TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
; TITLE OF INVENTION: Encoding Sequence Therefor
; Patent No. 5840577
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462.481
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,086
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-481-4

Query Match 13.2%; Score 224; DB 2; Length 679;
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHGHAQSAALQKVKQGERVKTSLDLRREIDVCGIONLIE-----LRKKRQ 93
DB 22 VVEDD-----SSLKAVQKGDVVRV-----QQLLEKADANACEDTGWTFPLHNAVQA 69
QY 94 KKRD--LAASHEPPPEPEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCDO--- 148
DB 70 GRVDIVNLLSHGADPHRRKKNGAT---PFIAGIQGDVKLLLEILSCGADVNECDNGF 126
QY 149 -----FRR-----TALHRASLEGHMEILEK 168

Db 127 TAFMEAAERGAELRFLFAKGANVNLRRQTTKDKRRLLKQGGATALMSAAEKGHLEVLRI 186
QY 169 LL-DNGATVDFODR-----LDCATAMHWACRGHLEVVKLLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDMKAEDVARDNMGRLNIRTLNWDCEVNE-EITSILIOHGADVNVVRGERTPLIA 245
QY 223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDVRLNRYKIKLLLLHGGADMMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARDNEGTALLIAVDKOLKEIVOLLLEKGDAC----- 300
QY 282 GKTPTDLVOLWQADTRH 298
Db 301 ----DDLVL-WIARRNH 311

RESULT 7

US-08-436-771-6
; Sequence 6, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-436-771-6

Query Match 13.2%; Score 224; DB 2; Length 679;
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHGAQSAALQKVGQERVRTSLDLREITDVGIGIQLIE-----LRKKRQ 93
Db 22 VVEDD-----SSLKAVQKGVVRY-----QOLLEKADANACEDTGWTPPLHNAVOA 69
QY 94 KKRD--LAASHEPPPEPEITGPVDEETFLKAAVGGKMKVIEKFLADGSGADTCQD--- 148
Db 70 GRVDIVNLLSHGADPHRRKNGAT---PFITAGIOGVKLLLEILLSCGADVNECDENG 126

QY 149 -----FRR-----TALHRASLEGHMEILEK 168
Db 127 TAFMEAAERGAELRFLFAKGANVNLRRQTTKDKRRLLKQGGATALMSAAEKGHLEVLRI 186
QY 169 LL-DNGATVDFODR-----LDCATAMHWACRGHLEVVKLLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDMKAEDVARDNMGRLNIRTLNWDCEVNE-EITSILIOHGADVNVVRGERTPLIA 245
QY 223 AVRTGQVEIVEHFLSL-GLEINARDREGDTALHDVRLNRYKIKLLLLHGGADMMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARDNEGTALLIAVDKOLKEIVOLLLEKGDAC----- 300
QY 282 GKTPTDLVOLWQADTRH 298
Db 301 ----DDLVL-WIARRNH 311

RESULT 8

US-08-434-998-6
; Sequence 6, Application US/08434998
; Patent No. 5866781
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/434,998
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-434-998-6

Query Match 13.2%; Score 224; DB 2; Length 679;
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHGAQSAALQKVGQERVRTSLDLREITDVGIGIQLIE-----LRKKRQ 93
Db 22 VVEDD-----SSLKAVQKGVVRY-----QOLLEKADANACEDTGWTPPLHNAVOA 69
QY 94 KKRD--LAASHEPPPEPEITGPVDEETFLKAAVGGKMKVIEKFLADGSGADTCQD--- 148

Db 70 GRVDIVNLLSHGADPHRRKKNKAT---PFIITAGIQGDVKLLLEILLSCGADVNECDNGF 126
QY 149 -----FRR-----TALHRASLEGHMEILEK 168
Db 127 TAFMEAERGNAELRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
QY 169 LL-DNGATVDFQDR-----LDCATAMHWACRGHLEVVKLLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDMKAEDVARDNMGRLNIRTLNWDCEVNE-BITSILIOHGADVNVVRGKGTPLIA 245
QY 223 AVRTQGVVEIHFSL-GLEINARDREGDTALHDVRLNRYKIIKLLHGHGADMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARNEGKTALLIAVDKOLKEIVQLLLEKGDAC----- 300
QY 282 GKTPDVLQVMOQADTRH 298
Db 301 ----DDL-V-WIARRNH 311

RESULT 9
US-08-487-797-6
; Sequence 6, Application US/08487797
; Patent No. 5866787
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Transgenic Plants Co-Expressing A
; TITLE OF INVENTION: Functional Human 2-5A System
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Holland & Knight
; STREET: One E. Broward Boulevard, #1300
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,797
; FILING DATE: 07-JUNE-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16(C)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/468-7811
; TELEFAX: 305/463-2030
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-797-6

Query Match 13.2%; Score 224; DB 2; Length 679;
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHHGAQAALQKVGQERVKTSLDLRREIDVGGIONLIE-----LRKKRQ 93
Db 22 VVEDD-----SSLKAVQKGVVRY-----QQLLEKGDANACEDTGWTPPLHNAVOA 69
QY 94 KKRDA--LAASHEPPEPEITGPVDEETFLKAAVEGKMKVTEKFLADGSGADTCDQ--- 148
Db 70 GRVDIVNLLSHGADPHRRKKNKAT---PFIITAGIQGDVKLLLEILLSCGADVNECDNGF 126

QY 149 -----FRR-----TALHRASLEGHMEILEK 168
Db 127 TAFMEAERGNAELRFLFAKGANVNLRRQTTKDKRRLKQGGATALMSAAEKGHLEVLRI 186
QY 169 LL-DNGATVDFQDR-----LDCATAMHWACRGHLEVVKLLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDMKAEDVARDNMGRLNIRTLNWDCEVNE-BITSILIOHGADVNVVRGKGTPLIA 245
QY 223 AVRTQGVVEIHFSL-GLEINARDREGDTALHDVRLNRYKIIKLLHGHGADMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARNEGKTALLIAVDKOLKEIVQLLLEKGDAC----- 300
QY 282 GKTPDVLQVMOQADTRH 298
Db 301 ----DDL-V-WIARRNH 311

RESULT 10
US-08-701-005A-4
; Sequence 4, Application US/08701005A
; Patent No. 5877019
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Almin
; TITLE OF INVENTION: Animal 2-5A-Dependent RNases and
; TITLE OF INVENTION: Encoding Sequence Therefor
; Patent No. 5877019
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz
; STREET: 555 - 13th Street, N.W., Suite 701 E
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/701,005A
; FILING DATE: 21-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/141,304
; FILING DATE: 22-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,086
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jondle, Robert J.
; REGISTRATION NUMBER: 33,915
; REFERENCE/DOCKET NUMBER: N1255-111
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-783-6040
; TELEFAX: 202-783-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-701-005A-4

Query Match 13.2%; Score 224; DB 2; Length 679;
Best Local Similarity 28.1%; Pred. No. 7.3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHHGAQAALQKVGQERVKTSLDLRREIDVGGIONLIE-----LRKKRQ 93

Db 22 VVEDD-----SSLIKAVQGDVVVR-----QOLLEKAGADANACEDTGWTPPLHNAVQA 69
QY 94 KKRDAA--LAASHEPPPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCQ--- 148
Db 70 GRDIVNLLSHGADPHRRKNGAT---PFIAGIQGDVKLLLEILLSCGADVNECDNGF 126
QY 149 -----FRR-----TALHRASLEGHMEILEK 168
Db 127 TAFMEAAERGAELRFLKAGANVNLRRQTTKDKRRLKQGGATALMSAAEKHLEVLRI 186
QY 169 LL-DNGATVDFODR-----LDCTAMHWACRGHLEVVVKKLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDKMAEVDARDMGRNALIRTLNWDCEVE-EITSILIQHGADVNVVRGERGKTPLIA 245
QY 223 AVRTGOVEIVEHFLSL-GLEINARDREGDTALHDVRLNRYKIIKILLHGHGADMMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARNEGKTALLIANDVKQLKEIVQLLEKGAADK 300
QY 282 GKPTDVLVQWQADTRH 298
Db 301 ----DDLW--WIARRNH 311

RESULT 11
US-08-479-895-4
; Sequence 4, Application US/08479895
; Patent No. 5972678
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Aimin
; TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
; TITLE OF INVENTION: Encoding Sequence Therefor
; Patent No. 5972678
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/479,895
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,086
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-13
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-479-895-4

Query Match 13.2%; Score 224; DB 2; Length 679;

Best Local Similarity 28.1%; Pred. No. 7 3e-14;
Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;
QY 41 VLEDEKHGAQSAALQKVKQGERKRTSLDLREIIVDVGIIQNLIE-----LRKKRKQ 93
Db 22 VVEDD-----SSLIKAVQGDVVVR-----QOLLEKAGADANACEDTGWTPPLHNAVQA 69
QY 94 KKRDAA--LAASHEPPPEEITGPVDEETFLKAAVEGKMKVIEKFLADGGSADTCQ--- 148
Db 70 GRDIVNLLSHGADPHRRKNGAT---PFIAGIQGDVKLLLEILLSCGADVNECDNGF 126
QY 149 -----FRR-----TALHRASLEGHMEILEK 168
Db 127 TAFMEAAERGAELRFLKAGANVNLRRQTTKDKRRLKQGGATALMSAAEKHLEVLRI 186
QY 169 LL-DNGATVDFODR-----LDCTAMHWACRGHLEVVVKKLQSHGADTVNRDKLLSTPLHV 222
Db 187 LNDKMAEVDARDMGRNALIRTLNWDCEVE-EITSILIQHGADVNVVRGERGKTPLIA 245
QY 223 AVRTGOVEIVEHFLSL-GLEINARDREGDTALHDVRLNRYKIIKILLHGHGADMMTKNLA 281
Db 246 AVERKHTGLVQMLLSREGINIDARNEGKTALLIANDVKQLKEIVQLLEKGAADK 300
QY 282 GKPTDVLVQWQADTRH 298
Db 301 ----DDLW--WIARRNH 311

RESULT 12
PCT-US95-02058-6
; Sequence 6, Application PC/TUS9502058
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: SenGupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02058
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CL11363-16
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 679 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-02058-6

Query Match 13.2%; Score 224; DB 5; Length 679;
 Best Local Similarity 28.1%; Pred. No. 7.3e-14;
 Matches 89; Conservative 41; Mismatches 101; Indels 86; Gaps 13;

QY 41 VLEDEKHAQSAALQVKGOERVKTSLSLRLRETIIDVGGIONLIE-----LRKKRQ 93
 Db 22 VVEDD-----SSLKAVQKGDVVRV-----QQLERKADANACEDTWGTPPLHNAVQA 69
 QY 94 KKRA--LAASPEPEPEETGPVDEETFLKAAVEGRMKVIEKFLADGSDATCDQ--- 148
 Db 70 GRVDIVLLSHGADPHRRKNGAT--PFIAGIQGDVKKLEILLSCGADVNECDENG 126
 QY 149 -----FRR-----TALHRASLEGHMEILEK 168
 Db 127 TAFMEAERGNALRFLFAKGANVLRQTTKDRRLKQGGATALMSAAEKHLEVLRI 186
 QY 169 LL-DNGATVDFQDR-----LDCTAMHWACRGHLEVVKLLQSHGADTNVRKLLSTPLHV 222
 Db 187 LNDKMAEVDARDNMGRLITLLNWCENVE-BITSILQHGADVNRGERGKTPLIA 245
 QY 223 AVRTGQVIEVHEFLSL-GLEINARDREGDTALHDVRLNRYKIIKLLLLHGADMMTKNLA 281
 Db 246 AVERKHTGLVQMLLSREGINARDNECKTALLIADVQKLEIVQLLEKADKC----- 300

QY 282 GKTPTDLVQLWQADTRH 298
 Db 301 ----DDLV--WTARRNH 311

RESULT 13
 US-08-484-575A-6
 ; Sequence 6, Application US/08484575A
 ; Patent No. 5925358
 ; GENERAL INFORMATION:
 ; APPLICANT: Mark D. Cochran and David E. Junker
 ; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
 ; NUMBER OF SEQUENCES: 42
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John P. White
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,575A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White Esq, John P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)278-0450
 ; TELEFAX: (212)391-0525
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 422 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-484-575A-6

Query Match 13.2%; Score 223; DB 2; Length 422;
 Best Local Similarity 25.9%; Pred. No. 4.6e-14;
 Matches 67; Conservative 48; Mismatches 98; Indels 46; Gaps 7;

QY 68 SLDLRLREII--DVGGIONLIELRKKRKKRDALAAASHEPPEPEITGPVDEETFLKAA 125
 Db 68 SLDLRLREII--DVGGIONLIELRKKRKKRDALAAASHEPPEPEITGPVDEETFLKAA 125

Db 2 SVDWRTIYSGDISLVEKLI-----KNKGNCINIS-----VEETTPPL-----IDAI 43
 QY 126 VEGKMKVIEKFLADGGSADTCD-QFRRTALHRASLEGH----- 162
 Db 44 RTGNAKIVELFKHGAQVNHVNTKIPNPLLTAKIGSHDIVKLLINGVDTSLPVPICIN 103
 QY 163 MEILEKLDNGATVDFQDRLDCTAMHWACRGHLEVVKLLQSHGADTNVRKLLSTPLHV 222
 Db 104 KEMIKTILDSGVKVNKNAKSKTFLHYAIAKNNDLEVIKMLFEYGADVNIKDDNICYSIHI 163
 QY 223 AVRTGQVIEVHEFLSLGLEINARDREGDTALHDVRLNRYKIIKLLLLHGADMMTKNLA 282
 Db 164 ATRSNYSYELIKLLLEKGAIVANVKNYNSPLHNAAYGDIYACIKLVLDHTNINSKNCNG 223
 QY 283 KTPTDLVQLWQADTRHALE 301
 Db 224 VTPLHNALY---NESAVE 239

RESULT 14
 US-08-477-459-6
 ; Sequence 6, Application US/08477459
 ; Patent No. 6001369
 ; GENERAL INFORMATION:
 ; APPLICANT: Mark D. Cochran
 ; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: John P. White
 ; STREET: 1185 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/477,459
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: White Esq, John P
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 278-0400
 ; TELEFAX: (212) 391-0525
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 422 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-477-459-6

Query Match 13.2%; Score 223; DB 3; Length 422;
 Best Local Similarity 25.9%; Pred. No. 4.6e-14;
 Matches 67; Conservative 48; Mismatches 98; Indels 46; Gaps 7;

QY 68 SLDLRLREII--DVGGIONLIELRKKRKKRDALAAASHEPPEPEITGPVDEETFLKAA 125
 Db 2 SVDWRTIYSGDISLVEKLI-----KNKGNCINIS-----VEETTPPL-----IDAI 43
 QY 126 VEGKMKVIEKFLADGGSADTCD-QFRRTALHRASLEGH----- 162
 Db 44 RTGNAKIVELFKHGAQVNHVNTKIPNPLLTAKIGSHDIVKLLINGVDTSLPVPICIN 103
 QY 163 MEILEKLDNGATVDFQDRLDCTAMHWACRGHLEVVKLLQSHGADTNVRKLLSTPLHV 222
 Db 104 KEMIKTILDSGVKVNKNAKSKTFLHYAIAKNNDLEVIKMLFEYGADVNIKDDNICYSIHI 163

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OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 08:09:16 ; Search time 88.05 Seconds
(without alignments)
2978.552 Million cell updates/sec

Title: US-09-758-593A-2
Perfect score: 1158
Sequence: 1 cagctcgaggagcgaccac.....ctaccacaataaaaagctg 1158

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	77.2	6.7	1288	US-09-172-977-2	Sequence 2, Appli
2	75.6	6.5	3454	US-09-082-059-1	Sequence 1, Appli
3	64.2	5.5	1789	US-09-035-706-1	Sequence 1, Appli
4	64.2	5.5	1789	US-08-955-841-1	Sequence 1, Appli
5	64.2	5.5	1789	US-09-428-219-3	Sequence 3, Appli
6	62.4	5.4	16442	US-08-781-891-208	Sequence 208, App
7	62	5.4	4134	US-09-196-387-1	Sequence 1, Appli
8	62	5.4	4491	US-09-196-387-7	Sequence 7, Appli
9	61.8	5.3	2928	US-08-462-481-1	Sequence 1, Appli
10	61.8	5.3	2928	US-08-436-771-1	Sequence 1, Appli
11	61.8	5.3	2928	US-08-436-771-3	Sequence 3, Appli
12	61.8	5.3	2928	US-08-434-998-1	Sequence 1, Appli
13	61.8	5.3	2928	US-08-434-998-3	Sequence 3, Appli
14	61.8	5.3	2928	US-08-487-797-1	Sequence 1, Appli
15	61.8	5.3	2928	US-08-487-797-3	Sequence 3, Appli
16	61.8	5.3	2928	US-08-701-005A-1	Sequence 1, Appli
17	61.8	5.3	2928	US-08-479-895-1	Sequence 1, Appli
18	61.8	5.3	2928	PCT-US95-02058-1	Sequence 1, Appli
19	61.8	5.3	2928	PCT-US95-02058-3	Sequence 3, Appli
20	61.8	5.3	2931	US-08-943-956A-1	Sequence 1, Appli
21	61.2	5.3	4935	US-08-631-097-3	Sequence 3, Appli
22	61.2	5.3	5886	US-08-810-712-9	Sequence 9, Appli
23	60.6	5.2	3516	US-09-188-930-257	Sequence 257, App
24	59.4	5.1	4657	US-09-196-387-9	Sequence 9, Appli
25	59.4	5.1	7218	US-08-232-463-14	Sequence 14, Appli
26	58.6	5.1	2580	US-09-050-863-2	Sequence 2, Appli
27	58.6	5.1	5452	US-09-130-114-1	Sequence 1, Appli

28	58.6	5.1	9600	4	US-08-910-647-1	Sequence 1, Appli
29	58.6	5.1	10596	1	US-07-884-811-15	Sequence 15, Appl
30	58.6	5.1	10596	1	US-07-885-971-15	Sequence 15, Appl
31	58.6	5.1	10596	1	US-08-087-783A-15	Sequence 15, Appl
32	58.6	5.1	10596	1	US-08-194-088B-15	Sequence 15, Appl
33	58.6	5.1	10596	2	US-08-194-087-15	Sequence 15, Appl
34	58.6	5.1	10596	2	PCT-US93-04848-15	Sequence 15, Appl
35	55.4	4.8	2200	2	US-08-462-481-3	Sequence 3, Appli
36	55.4	4.8	2200	2	US-08-436-771-5	Sequence 5, Appli
37	55.4	4.8	2200	2	US-08-434-998-5	Sequence 5, Appli
38	55.4	4.8	2200	2	US-08-487-797-5	Sequence 5, Appli
39	55.4	4.8	2200	2	US-08-701-005A-3	Sequence 3, Appli
40	55.4	4.8	2200	2	US-08-479-895-3	Sequence 3, Appli
41	55.4	4.8	2200	3	PCT-US95-02058-3	Sequence 3, Appli
42	55.4	4.8	2200	5	PCT-US95-02058-5	Sequence 5, Appli
43	54.8	4.7	3489	2	US-08-728-323A-1	Sequence 1, Appli
44	54.8	4.7	32207	2	US-08-770-379-20	Sequence 20, Appl
45	54.8	4.7	32207	4	US-08-757-669A-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-172-977-2
; Sequence 2, Application US/09172977
; Patent No. 5989863
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: HUMAN ANKYRIN FAMILY PROTEIN
; FILE REFERENCE: PF-0615 US
; CURRENT APPLICATION NUMBER: US/09/172,977
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1288
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 1808075
US-09-172-977-2

Query Match	6.7%	Score 77.2;	DB 2;	Length 1288;
Best Local Similarity	48.2%	Pred. No. 2.4e-10;		
Matches 217;	Conservative	0;	Mismatches 233;	Indels 0; Gaps 0;
QY	435	acgggggggtcagccgacacgtgcgaccagtccgtcgagacagcactgcaccgagcttccc	494	
DB	589	acgaggtgtcagctgtgcgcgcacccctcctgagcactcctgcacacagctgcgcagac	648	
QY	495	tggaggccacatgaaatccttggaagacttctagataatggggccactgtggaacttcc	554	
DB	649	aggggagctgagcagctggaagagcatttcggaaggtgacacccctcgcaacagc	708	
QY	555	aggatcgctgactgcacagcactgcatggcctccgcgcggggccacttagaggtgg	614	
DB	709	cagcagcgcgcgttccacccctcctcctggtcccttccttggagagattgagacgc	768	
QY	615	tgaactcttgcacacccatggagcagacacccaatgtgaggataagctgctgagaccc	674	
DB	769	ttcgtctctgtgagtggtggtgcgcacccacacatcctggcaaaagcagagagagcg	828	
QY	675	cgtgcacgtgcagtcgcgcagggcagggcaggtgtgagacatttgcacatttctatccctgg	734	
DB	829	cctgtcgctggtccagcagcgcgctacacagacattgtgggggtgctgtggagcgtg	888	
QY	735	gctggaatcattgcagcagacaggggaggggatactgacctgcatgacgctgtgagcg	794	

Db 889 acgtggacatcaacatctatgattggaatggaggagccactgctgtacgtgtgctg 948
QY 795 tcaacgcgtacaaaatcatcaactgctctcctgcatgggactgaacatgacacaaga 854
Db 949 ggaacacacgtgaatgctgtggtgctctgctgcccggagcgctgacctcacacacgaag 1008
QY 855 acctggcaggaagaccccgacggacctgg 884
Db 1009 ccgactctgctacaccccgatggaccttg 1038

RESULT 2

US-09-082-059-1
; Sequence 1, Application US/09082059A
; Patent No. 6225086
; GENERAL INFORMATION:
; APPLICANT: Morrow, Jon S.
; APPLICANT: Devarajan, Prasad
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identification
; FILE REFERENCE: 44574-5002-US
; CURRENT APPLICATION NUMBER: US/09/082,059A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/047356
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(3394)
; OTHER INFORMATION: DNA/protein segment- human kidney Ankyrin G119
US-09-082-059-1

Query Match 6.5%; Score 75.6; DB 4; Length 3454;
Best Local Similarity 47.5%; Pred. No. 8.2e-10;
Matches 225; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 378 ccttctgaaagctgcgtggaggagaaatgaagtcattgagaagttcctggctgacg 437
Db 993 ccgtccatctcagctcaggaaggagcgatgacatggtcgtcgtcctcgttagaa 1052
QY 438 ggggtgcagccagacgctgcgacacttcctgcggacagcactgcacgactccctgg 497
Db 1053 atgcgaatgtgaacctgagcaataagagcggtcgtgacccactccattggtgtctcaag 1112
QY 498 aaggccacatggaatcctggagaagcttctagataatgggcccactgtggacttcacgg 557
Db 1113 aagatcgagtgaatgtggcagaagctcgttaaaccaagggtcctatgtggagcccca 1172
QY 558 atcggctgactgcacagcactgattggcctgcgcgggggccaacttagaggtggtga 617
Db 1173 caaagatgggatacacacacacactgcatgtgggtgcacatggaataatcaagattgta 1232
QY 618 aactctgcaagccatgagcagacacacaaatgtgaggatgaagctgctgagcaccgcc 677
Db 1233 atttctgtccagcattctgcaaaatgaatgcaaaacaaagaatgggtatagccat 1292
QY 678 tgcacgtggcgtccggacagggaggtgagattgtgagcactttctatccctgggcc 737
Db 1293 tacataagcagcagcaggggcatacgcataataaatgtcttacttcagaacaag 1352
QY 738 tggaaatcaatccagagacagggaggaatactgacctgcatgacgtgtgagctca 797
Db 1353 cctcccccaatgaactcaactgtgaatgggaatactgacctggcattgcccggcgctcg 1412
QY 798 accgctacaaaatcatcaaacgtctcctcgtcgtcgtgaggtgacatgatgacca 851
Db 1413 gctacatctcagtagtggaacccctggaagatagtgaccgaagaacacatgacca 1466

RESULT 3

US-09-035-706-1
; Sequence 1, Application US/09035706
; Patent No. 6001622
; GENERAL INFORMATION:
; APPLICANT: Dedhar, Shoukat
; APPLICANT: Hannigan, Greg
; TITLE OF INVENTION: Integrin-Linked Kinase and
; TITLE OF INVENTION: its Uses
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bozicevic & Reed, LLP
; STREET: 285 Hamilton Avenue, Suite 200
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/035.706
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sherwood, Pamela J
; REGISTRATION NUMBER: 36,677
; REFERENCE/DOCKET NUMBER: KIN-2CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-327-3400
; TELEFAX: 650-327-3231
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-035-706-1

Query Match 5.5%; Score 64.2; DB 3; Length 1789;
Best Local Similarity 49.8%; Pred. No. 4.5e-07;
Matches 162; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

QY 556 ggaatcggtgactgcacagccatggtggcctgcccggggccacttagagtggt 615
Db 246 GGACCATATGGCTTCTCCCCCTTGACATGGGCGCTGCCGAGAGGCGCGCTGTGTGTGT 305
QY 616 gaaactctgcaaaagcattggagcagacacccaatgtgagggaataagctgctgagcacc 675
Db 306 TCAGATGTTGATCATCGGGGGGCGACGATCAATGTAATGAACCGTGGGGATGACACCCC 365
QY 676 gctgacgtggcagtcggacagggcaggtggagattgtggagcactttctatccctggg 735
Db 366 CCGTGCATCTGGCAGCAGTCATCGACACCGCTGATATTGTACAGAAAGCTATTGCACTACAA 425
QY 736 cctgaaatcaatgcacagagacaggggaaggaatactgctcctgcatgagcgtgtgaggt 795
Db 426 GCACACATCAATGAGTGAATGAACACGGGAATGCGCCCTGCACTATGCTCTGTTTGTG 485
QY 796 caacgctacaaaatcatcaaaactgctcctgcatgggggctgacatgatgaccaaga 855
Db 486 GGGCCAAGATCAAGTGGCAGAGGACCTGTGTGCAAAATGGGCCCCCTTGTGACGATCTGTAA 545
QY 856 cctggcaggaagaccccgacggac 880

STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-781-891-208

Query Match 5.4%; Score 62.4; DB 3; Length 16442;

Best Local Similarity 51.0%; Pred No. 2.6e-06;

Matches 147; Conservative 0; Mismatches 141; Indels 0; Gaps 0;

QY 22 ggaggactccgaggggtgcagagggccacagcgtctcagcagcggcgtgcacagga 81
DB 16412 GGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 16353
QY 82 ggaggaatgaaactccgaggaacacacagcagcagcagcagcagcagcagcagc 141
DB 16352 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 16293
QY 142 gctggaggatgagaagcaccacggggctcagagtgccagcagcagcagcagcagc 201
DB 16292 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA 16233
QY 202 agagcgtgcgaagcgtccctgacgtgcggcgaggagatcatcgtggtggcgagat 261
DB 16232 GGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAA 16173
QY 262 ccagaacctcatcagctgcgggaagaaacgcaagcagcagcagcagcagcagc 309
DB 16172 GAAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGACAGAA 16125

RESULT 7

US-09-196-387-1

; Sequence 1, Application US/09196387

; Patent No. 6277613

; GENERAL INFORMATION:

; APPLICANT: de Lange, Titia

; APPLICANT: Smith, Susan

; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

; TITLE OF INVENTION: OF USE THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue, 4th Floor

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 09/095,225
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
US-09-196-387-1

Query Match 5.4%; Score 62; DB 4; Length 4134;

Best Local Similarity 49.7%; Pred. No. 2.1e-06;

Matches 158; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 567 actgcacagccatgcattggcctccgcggggccacttagaggtggtgaactctgc 626
DB 2515 ATTCAACCCCTTGGACCTGGCAGGAGGCTATAATAACCTGGAAGTAGTGAATATCTTC 2574
QY 627 aaagccatggagcagacacccaatgtgaggataaagctgctgagcaccgcgtgcacgtgg 686
DB 2575 TAGACATGGAGCTGATGTAATGCCAGACAAAGGTGGTTAATTCCTCTTCAATG 2634
QY 687 cagtcggagacagggcaggtggagattgtgagcaactttctatccctgggctggaaatca 746
DB 2635 CGGCATCTTATGGCATGTGTGACATAGCGGCTTTATTGATAAATAACACACGCTGTGTAA 2694
QY 747 atgcagagacaggaaggggatactgccctgcagcagcgtgtgaggtccaaccgtaca 806
DB 2695 ATGCAACAGATAGTGGGGCTTTACTCCCTCCATGAACAGCAGCCAGAGGAGGAGCGC 2754
QY 807 aaatcatcaactgctgctcctgcagtgagggtgggctgacatgatgacccaagaacctggcaggaa 866
DB 2755 AGCTGTGCGCCCTCTCTCTAGCGCATGTGTCAGACCCCATGAAGAACCCAGGAAGGCC 2814
QY 867 agaccocagcggacctgg 884
DB 2815 AGACGCTCTGGATCTGG 2832

RESULT 8

US-09-196-387-7

; Sequence 7, Application US/09196387

; Patent No. 6277613

; GENERAL INFORMATION:

; APPLICANT: de Lange, Titia

; APPLICANT: Smith, Susan

; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS

; TITLE OF INVENTION: OF USE THEREOF

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue, 4th Floor

; CITY: Hackensack

; COMPUTER READABLE FORM:

STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196.387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 6..2027
US-09-196-387-7

Query Match 5.4%; Score 62; DB 4; Length 4491;
Best Local Similarity 49.7%; Pred. No. 2.2e-06;
Matches 158; Conservative 0; Mismatches 160; Indels 0; Gaps 0;

QY 567 actgacagcctatgattggcctgcccgggggccacttagaggtggtaacctctgc 626
DB 2872 ATTCAACCCCTCTGCACCTGGCAGCGCTATATAACCTGGAACTAGCTGAATCTTC 2931
QY 627 aaagccatgagcagacacccaatgagggataaagctgtgagcaccgcgtgcactgg 686
DB 2932 TAGAGCATGGAGCTGATGTTAATGCCAGCAAGGGTGTAAATTCCTCTTCAATG 2991
QY 687 cagtcggacagggcaggtggagattgtgagcactttctatccctggcctggaaatca 746
DB 2992 CGGCATCTTATGGCATGTTGACATAGCGCTTTATTGATAAAATACACACGTGTGTAA 3051
QY 747 atgcagagacaggaaggggatactgcccctgcatgacgctgtgaggtccaaccgtaca 806
DB 3052 ATGCAACAGATAAGTGGGCGTTTACTCCCTCCATGAAGCAGCCCAAGAAAGGACGC 3111
QY 807 aatcatcaaaactgctcctcctgctgagctgacatgacacgaagacccctggcaggaa 866
DB 3112 ACTGTGCGCCCTCTCTCTAGCGCATGGTGGACAGCCCAACCCCATGTAAGAAACCAAGAGGCC 3171
QY 867 agaccgccgagcactgg 884
DB 3172 AGACGCCCTCTGGATCTGG 3189

RESULT 9
US-08-462-481-1
; Sequence 1, Application US/08462481
; Patent No. 5840577
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.

APPLICANT: Zhou, Almin
TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
Patent No. 5840577
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
ADDRESS: Russell
CITY: 200 East Broward Boulevard
STATE: Florida
COUNTRY: USA
ZIP: 33301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462.481
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,086
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: CL11363-13
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305/527/2498
TELEFAX: 305/764/4996
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2928 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 104..2326
US-08-462-481-1

Query Match 5.3%; Score 61.8; DB 2; Length 2928;
Best Local Similarity 57.8%; Pred. No. 2.1e-06;
Matches 130; Conservative 0; Mismatches 92; Indels 3; Gaps 1;

QY 616 gaaactctgcaaaagccatggagcagacacccaatgtgaggataaagctgtgagcacc 675
DB 769 GCATCTGCTGCTGGACCATGGGCTGATGTCATGAGGGAGAGAGGAGAGACTCC 828
QY 676 gctgcacgtggcagtcgccgagcagggcaggtgagagtgtgagcactttctatccctgg 735
DB 829 CTTGATCTCTGGCAGTGGAGAGAACACTTGGGTTTGGTGCAGAGGCTTCTGGAGCAAGA 888
QY 736 cc---tggaatacaatgccagagacaggaaggggatactgcccctgcatgacgctgtgag 792
DB 889 GCACATAGAGATTAAATGACACAGACAGATGATGGCAAAACAGCACTGCTGCTCTGTGA 948
QY 793 gctcaaccgctcaaaatcatcaaaactgctgctcctgcatggggc 837
DB 949 ACTCAAACTGAAGAAAATCGCCGAGTTGCTGTGCAAAACCTGGAGC 993

RESULT 10
US-08-436-771-1
; Sequence 1, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.

;; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
;; TITLE OF INVENTION: Cells and Methods
;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;; ADDRESSEE: Russell
;; STREET: 200 E. Broward Boulevard
;; CITY: Fort Lauderdale
;; STATE: Florida
;; COUNTRY: USA
;; ZIP: 33301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,771
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/198,973
;; FILING DATE: 18-FEB-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Manso, Peter J.
;; REGISTRATION NUMBER: 32,264
;; REFERENCE/DOCKET NUMBER: CL11363-16
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 305/527/2498
;; TELEFAX: 305/764/4996
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2928 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 104...2326
;; US-08-436-771-1

Query Match 5.3%; Score 61.8; DB 2; Length 2928;
Best Local Similarity 57.8%; Pred. No. 2.1e-06;
Matches 130; Conservative 0; Mismatches 92; Indels 3; Gaps 1;
QY 616 gaaacttctgcaagccatggagacacacccaatgtgagggataaagctgctgagaccccc 675
Db 769 GCATCTGCTGCTGGACCATGGGCTGATGTCATATGTGAGGGGAGAAAGAGGGAAGACTCC 828
QY 676 gctgcacgtgagctccgagacagggcagggtggagattgtgagcactttctatccctggg 735
Db 829 CCTGATCTGGCAGTGGAGAGAGCACTTGGTTGGTTCAGAGGCTTCTGGAGCAAGA 888
QY 736 cc---tggaataatccagagacaggggaaggggatactgcccctgcatgacgtgtgag 792
Db 889 GCATATAGAGATTAAATGACACAGACAGTGTGATGCAAAACAGACACTGCTGCTGCTTGA 948
QY 793 gctcaaccgctacaaatacatcaactgctcctcctgcatggggc 837
Db 949 ACTCAAACTGAAGAAATCCCGAGTTGCTGTGCAAAACGTGGAGC 993

RESULT 11
US-08-436-771-3
; Sequence 3, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods

;; NUMBER OF SEQUENCES: 11
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
;; ADDRESSEE: Russell
;; STREET: 200 E. Broward Boulevard
;; CITY: Fort Lauderdale
;; STATE: Florida
;; COUNTRY: USA
;; ZIP: 33301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/436,771
;; FILING DATE:
;; CLASSIFICATION: 536
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/198,973
;; FILING DATE: 18-FEB-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Manso, Peter J.
;; REGISTRATION NUMBER: 32,264
;; REFERENCE/DOCKET NUMBER: CL11363-16
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 305/527/2498
;; TELEFAX: 305/764/4996
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2928 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 104...2326
;; US-08-436-771-3

Query Match 5.3%; Score 61.8; DB 2; Length 2928;
Best Local Similarity 57.8%; Pred. No. 2.1e-06;
Matches 130; Conservative 0; Mismatches 92; Indels 3; Gaps 1;
QY 616 gaaacttctgcaagccatggagacacacccaatgtgagggataaagctgctgagaccccc 675
Db 769 GCATCTGCTGCTGGACCATGGGCTGATGTCATATGTGAGGGGAGAAAGAGGGAAGACTCC 828
QY 676 gctgcacgtgagctccgagacagggcagggtggagattgtgagcactttctatccctggg 735
Db 829 CCTGATCTGGCAGTGGAGAGCACTTGGTTGGTTCAGAGGCTTCTGGAGCAAGA 888
QY 736 cc---tggaataatccagagacaggggaaggggatactgcccctgcatgacgtgtgag 792
Db 889 GCATATAGAGATTAAATGACACAGACAGTGTGATGCAAAACAGACACTGCTGCTGCTTGA 948
QY 793 gctcaaccgctacaaatacatcaactgctcctcctgcatggggc 837
Db 949 ACTCAAACTGAAGAAATCCCGAGTTGCTGTGCAAAACGTGGAGC 993

RESULT 12
US-08-434-998-1
; Sequence 1, Application US/08434998
; Patent No. 5866781
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Sengupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ADDRESSEE: Russell
 STREET: 200 E. Broward Boulevard
 CITY: Fort Lauderdale
 STATE: Florida
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434,998
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/198,973
 FILING DATE: 18-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: CL11363-16
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305/527/2498
 TELEFAX: 305/764/4996
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2928 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 104..2326
 US-08-434-998-1

Query Match 5.3%; Score 61.8; DB 2; Length 2928;
 Best Local Similarity 57.8%; Pred. No. 2.1e-06;
 Matches 130; Conservative 0; Mismatches 92; Indels 3; Gaps 1;
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 Db 769 GCATCTGCTGTCGGACCATGGGCTGATGTCATGTGAGGGGAGAAAGAGGAGACTCC 828
 Qy 676 gctgcacgtggcagtcgcgacagagggcaggtgagattgtgagacactttctatccctggg 735
 Db 829 CCTGATCTGTCAGTGGAGAGAGACACTTGGGTTGGTGCAGAGGCTTCTGGAGCAAGA 888
 Qy 736 cc---tggaaatcaatgccagacagaggaaggataactgcccctgcatgacgctgtgag 792
 Db 889 GCACATAGAGATTATGACACAGACAGTGTGCAAAACAGACACTGCTGCTGCTTTGA 948
 Qy 793 gctcaacgcgtacaaaatcatcaaaactgctgctcctgcagtggggc 837
 Db 949 ACTCAAACTGAAGAAATCGCGAGTTGCTGTGCAAAACGTGGAGC 993

RESULT 13
 US-08-434-998-3
 ; Sequence 3, Application US/08/434998
 ; Patent No. 5866781
 ; GENERAL INFORMATION:
 ; APPLICANT: Silverman, Robert H.
 ; APPLICANT: Sengupta, Dibyendu N.
 ; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
 ; NUMBER OF INVENTIONS: Cells and Methods
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
 ; ADDRESSEE: Russell

STREET: 200 E. Broward Boulevard
 CITY: Fort Lauderdale
 STATE: Florida
 COUNTRY: USA
 ZIP: 33301
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/434,998
 FILING DATE:
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/198,973
 FILING DATE: 18-FEB-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Manso, Peter J.
 REGISTRATION NUMBER: 32,264
 REFERENCE/DOCKET NUMBER: CL11363-16
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 305/527/2498
 TELEFAX: 305/764/4996
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2928 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 104..2326
 US-08-434-998-3

Query Match 5.3%; Score 61.8; DB 2; Length 2928;
 Best Local Similarity 57.8%; Pred. No. 2.1e-06;
 Matches 130; Conservative 0; Mismatches 92; Indels 3; Gaps 1;
 Qy 616 gaaacttctgcaaaagccatgagcagacacccaattgtgaggataagctgctgagcacccc 675
 Db 769 GCATCTGCTGTCGGACCATGGGCTGATGTCATGTGAGGGGAGAAAGAGGAGACTCC 828
 Qy 676 gctgcacgtggcagtcgcgacagagggcaggtgagattgtgagacactttctatccctggg 735
 Db 829 CCTGATCTGTCAGTGGAGAGAGACACTTGGGTTGGTGCAGAGGCTTCTGGAGCAAGA 888
 Qy 736 cc---tggaaatcaatgccagacagaggaaggataactgcccctgcatgacgctgtgag 792
 Db 889 GCACATAGAGATTATGACACAGACAGTGTGCAAAACAGACACTGCTGCTGCTTTGA 948
 Qy 793 gctcaacgcgtacaaaatcatcaaaactgctgctcctgcagtggggc 837
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RESULT 14
 US-08-487-797-1
 ; Sequence 1, Application US/08/487797
 ; Patent No. 5866787
 ; GENERAL INFORMATION:
 ; APPLICANT: Silverman, Robert H.
 ; APPLICANT: Sengupta, Dibyendu N.
 ; TITLE OF INVENTION: Transgenic Plants Co-Expressing A
 ; NUMBER OF INVENTIONS: Functional Human 2-5A System
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Holland & Knight
 ; STREET: One E. Broward Boulevard, #1300
 ; CITY: Fort Lauderdale
 ; STATE: Florida

Search completed: April 17, 2002, 09:28:45
Job time: 4769 sec

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RESULT 15
US-08-487-797-3
; Sequence 3, Application US/08487797
; Patent No. 5866787
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GENERAL INFORMATION:
;
APPLICANT: Silverman, Robert H.
;
APPLICANT: Sengupta, Dibyendu N.
;
TITLE OF INVENTION: Transgenic Plants Co-Expressing A
;
TITLE OF INVENTION: Functional Human 2-5A System
;
NUMBER OF SEQUENCES: 11
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: Holland & Knight
;
STREET: One E. Broward Boulevard, #1300
;
CITY: Fort Lauderdale
;
STATE: Florida
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COUNTRY: USA
;
ZIP: 33301
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COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
;
OPERATING SYSTEM: PC-DOS/MS-DOS
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 08:09:16 ; Search time 175.48 Seconds
(without alignments)
5657.526 Million cell updates/sec

Title: US-09-758-593a-2
Perfect score: 1158
Sequence: 1 cagctcgaggagcgccacca.....ctaccacataaaaaagctg 1158

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

arched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /SID52/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1148.4	99.2	1208	22	AAI59509 Human polynucleoti
2	545.4	47.1	547	22	AAI61295 Human polynucleoti
3	248.4	21.5	1901	22	AAH02910 Human shear stress
4	192.8	16.6	221	21	AAC16163 Human secreted pro
5	113.4	9.8	386	22	AAF66063 Novel human polynu
6	103.8	9.0	363	22	AAH66048 Human polynucleoti
7	96.8	8.4	1783	22	AAI60004 Human polynucleoti
8	96.8	8.4	2894	22	AAI58218 Human polynucleoti
9	86.6	7.5	7185	22	AAH57380 Human skeletal mus
10	84.6	7.3	3040	22	AAH76497 Human ORFX ORF2052
11	79.2	6.8	2348	22	AAH46914 cDNA encoding huma

12	77.2	6.7	1288	21	AAZ49052 Human ankryrin fami
13	77.2	6.7	1345	21	AAZ94868 Human MHC class II
14	77.2	6.7	2649	19	AAV38678 Mus musculus SOCS1
15	75.6	6.5	3454	22	AAF83200 Human kidney ankyr
16	74	6.4	33654	22	AAF70259 Human dopamine rec
17	73.8	6.4	869	21	AAC76382 Human ORFX ORF1937
18	73.4	6.3	1959	22	AAH15018 Human cDNA sequenc
19	73.4	6.3	2790	21	AAZ36832 cDNA encoding a su
20	69.8	6.0	5482	22	AAF63955 Drosophila tankyria
21	68.2	5.9	1949	21	AAC77520 Human ORFX ORF3075
22	68.2	5.9	9063	22	AAH23688 Human tumour suppr
23	67	5.8	2499	22	AAS06739 Polynucleotide seq
24	67	5.8	3876	22	AAH15762 Human cDNA sequenc
25	65.8	5.7	1359	22	AAF90197 Nucleotide sequenc
26	65.6	5.7	1160	21	AAZ49069 Ankyrin repeat pro
27	65	5.6	6156	22	AAS01769 Drosophila melanog
28	65	5.6	24358	22	AAS01768 Drosophila melanog
29	64.8	5.6	1797	22	AAF90586 Degenerate DNA cod
30	64.8	5.6	1957	22	AAF90585 Human cDNA encoding huma
31	64.2	5.5	1780	20	AAZ33623 Human breast tumou
32	64.2	5.5	1786	18	AAT71716 Human integrin-lin
33	64.2	5.5	1789	22	AAF69274 Human integrin-lin
34	63	5.4	2157	18	AAT46188 Bovine Ribonucleas
35	62.8	5.4	1883	22	AAI59595 Human polynucleoti
36	62.4	5.4	16442	18	AAH83006 Partial mouse WRN
37	62.2	5.4	441	21	AAC69723 Human breast tumou
38	62.2	5.4	1773	22	AAH04776 Human death domain
39	62.2	5.4	2429	22	AAH35009 Human colon cancer
40	62.2	5.4	8091	19	AAV57001 Human Notch3 cDNA.
41	62	5.4	3984	22	AAF63838 Human tankyrase I
42	62	5.4	4134	21	AAC66826 Human tankyrase cD
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ALIGNMENTS

RESULT 1
AAI59509
ID AAI59509 standard; cDNA; 1208 BP.
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AC AAI59509;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 1712.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia; ss.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao QA, Zhou P, Goodrich R, Drmanac RT;

WPI; 2001-442253/47.
P-PSDB: AAM40353.

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -

claim 1: SEO ID NO 1712: 10078pp: English:

The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AA838642-AA842213) with neurotrophic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.

Note: The sequence data for this patent did not form part of the printed specification.

C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed specification.

Sequence 1208 BP: 292 A; 335 C; 392 G; 189 T; 0 other;

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Query Match          99.2%; Score 1148.4; DB 22; Length 1208;
Best Local Similarity 99.9%; Pred. No. 1.1e-267;
Matches 1149. Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 69 qqctqqcacaggaggaggaggaatgagaaactccgaggagagacacacgcccaggctgcccc 128

Db 99 ggctggcacaggaggaggaggaatgagaaactccgaggagacgcacgccaagtgccca 158

Qy 129 tggacttgctgctggaggatgagaagcaccacgggctcagagtgacagccctgcaga 188

Db 159 tggacttgctgctggaggatgagaagcaccacgggctcagagtgccagccctgcaga 218

189 aggtgaagggcccaagagcgctgcgcaagacgtccctggacctgcggcgaggatcatcg 248

Db 219 aggtgaaggccaagagcgcggtgcgcaagacgtccctggacctgcggcgaggatcatcg 278

Qy 249 atgtggcgggatccagaacctcatcgagctcgggaaagaaacgcaagcagaagaagcggg 308

Db 279 atgtggcgggatccagaacctcatcgagctcggaagaacgcaagcagaagaagcggg 338

Qy 309 acgctctggccgcctcgcctgatgagccgccccagagcccgaggagatcactggccctgtg 368

Db 339 acgctctggccgctcgcatgagccgccagagcccgaggagatcactggccctgtg 398

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Db 459 tggctgacgggggtcagccgacacgtgcgaccagtccgtcggacagcactgcaccgag 518

Qy 489 ctccctggaaggccacatggaatcctggagaagcttctagataatggggccactgtgg 548

Db 519 ctccctggaaggccacatggaatcctggagaagcttctagataatggggccactgtg 578

09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-OCT-2000; 2000US-0693036.
29-NOV-2000; 2000US-0727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
WPI; 2001-442253/47.
P-PSDB; AAM42139.
Novel nucleic acids and polypeptides, useful for treating disorders
such as central nervous system injuries -
Claim 1; SEQ ID NO 5284; 10078pp; English.
The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAM38642-AAM42213) with nootropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
specification.
SQ Sequence 547 BP; 132 A; 145 C; 195 G; 75 T; 0 other;

Query Match 47.1%; Score 545.4; DB 22; Length 547;
Best Local Similarity 99.8%; Pred. No. 2.3e-122;
Matches 546; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Dbb 1 gacggcaccatgagactccagagcggtgacagagggccacacgcgtcatcgagcagcg 60
Qy 71 ctggccacagggaggaggaatgagaaactccagagagacacacgcgcagaagctgcccatg 130
Dbb 61 ctggccacagggaggaggaatgagaaactccagagagacacacgcgcagaagctgcccatg 120
Qy 131 gacttgctggtgctgagagatgagacacacacggggtcagagtgccctgcagagaag 190
Dbb 121 gacttgctggtgctgagagatgagacacacacggggtcagagtgccctgcagagaag 180
Qy 191 gtgaagggccaaagagcggtgctgcagacgctccctggacctgcggcgagagatcatcgat 250
Dbb 181 gtgaagggccaaagagcggtgctgcagacgctccctggacctgcggcgagagatcatcgat 240
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Qy 491 tccctggaaaggccacatggaatactcctggagaagcttctagataatggggccactgtggac 550
Dbb 481 tccctggaaaggccacatggaatactcctggagaagcttctagataatggggccactgtggac 540
Qy 551 ttccagg 557
Dbb 541 ttccagg 547
RESULT 3
AAH02910
ID AAH02910 standard; DNA; 1901 BP.
XX
AC AAH02910;
XX
DT 15-JUN-2001 (first entry)
XX
DE Human shear stress-response coding sequence SEQ ID NO: 73.
XX
KW Human; shear stress-response protein; vascular disease;
arteriosclerosis; ds.
OS Homo sapiens.
XX
PN WO200125427-A1.
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-JP06840.
XX
PR 01-OCT-1999; 95JP-0280976.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
PA (NOJI/) NOJIMA H.
XX
PI Nojima H, Yoshisue H, Obayashi M, Ota T, Kawabata A, Sakurada K;
Kuga T, Sekine S, Nakamura Y, Sugano S;
XX
DR WPI; 2001-266308/27.
DR P-PSDB; AAB90787.
XX
PT DNA sequences, proteins encoded by them and antibodies against them
useful in diagnosis and treatment of vascular disease caused by
arteriosclerosis -
XX
PS Claim 20; Page 422-425; 678pp; Japanese.
XX
CC The present invention provides the protein and coding sequences of a
number of human shear stress response proteins. These are useful in the
diagnosis, treatment and screening of vascular diseases caused by
arteriosclerosis, including heart failure, post-PTCA restenosis and
hypertension.
XX
SQ Sequence 1901 BP; 592 A; 378 C; 460 G; 471 T; 0 other;
Query Match 21.5%; Score 248.4; DB 22; Length 1901;
Best Local Similarity 64.7%; Pred. No. 1.4e-50;
Matches 369; Conservative 0; Mismatches 201; Indels 0; Gaps 0;
Qy 338 ccagagcccgagagatcactggcctgtggatgagagacaccttctctgaagctgcggtg 397
Dbb 577 ccagagcccgagagatcactggcctgtggatgagagacaccttctctgaagctgcggtg 636
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Db 697 gatgagataaaacgacagctctctatagacatgcttgaagacatttggaattgtg 756
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 Db 1057 ctctctgattatgctgagcggagatctcaacatcaagaactgtgctgggaagacgcgatg 1116
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 Db 1117 gatctggtgtacactggcagaatggaacc 1146

RESULT 4

AAC16163
 ID AAC16163 standard; cDNA; 221 BP.
 XX AAC16163;
 AC AAC16163;
 DT 06-OCT-2000 (first entry)
 DE Human secreted protein 5' EST, SEQ ID NO: 20238.
 KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 PN EP1033401-A2.
 XX 06-SEP-2000.
 PF 21-FEB-2000; 2000EP-0200610.
 PR 26-FEB-1999; 99US-0122487.
 PA (GEST) GENSET.
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 PI WPI; 2000-500381/45.
 DR New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -
 XX Claim 1; SEQ ID 20238; 71pp + CD-ROM; English.
 PS The present sequence is one of a large number of 5' ESTs derived from
 CC mRNAs encoding secreted proteins. No ORF has yet been conclusively
 CC identified within the present sequence. The 5' ESTs were prepared from
 CC total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
 CC sequences usually correspond mainly to the 3' untranslated region (UTR)
 CC of the mRNA because they are often obtained from oligo-dT primed cDNA

CC libraries. Such ESTs are not well suited for isolating cDNA sequences
 CC derived from the 5' ends of mRNAs and even in those cases where longer
 CC cDNA sequences have been obtained, the full 5' UTR is rarely included.
 CC 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be
 CC used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used
 CC in diagnostic, forensic, gene therapy and chromosome mapping procedures.
 CC They are used to obtain upstream regulatory sequences and to design
 CC expression and secretion vectors.
 XX Sequence 221 BP; 54 A; 54 C; 87 G; 24 T; 2 other;

Query Match 16.6%; Score 192.8; DB 21; Length 221;
 Best Local Similarity 98.6%; Pred. No. 1.9e-37;
 Matches 205; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 8 agggcagccaccatggaggactcccgagcggtgcagaggccacagcgtctcatcagcag 67
 Db 11 atggacggccaccatggaggactcccgagcggtgcagaggccacagcgtctcatcagcag 70
 QY 68 cgctctggcacagagagagaaatgagaaactccgaggagacacacg-ccagaagctgcc 126
 Db 71 cggtctggcacagagagagaaatgagaaactccgaggagacacacg-ccagaagctgcc 130
 QY 127 catgacttctgctggtgaggtgagaaagcaccacggggtcagagtgagcagccctgca 186
 Db 131 catgacttctgctggtgaggtgagaaagcaccacggggtcagagtgagcagccctgca 190
 QY 187 gaagtgaaggccaaagagcgcgtgcgc 214
 Db 191 gaagtgaaggccaaagagcgcgtgcgc 218

RESULT 5

AAF66063
 ID AAF66063 standard; cDNA; 386 BP.
 XX AAF66063;
 AC AAF66063;
 DT 09-APR-2001 (first entry)
 DE Novel human polynucleotide, SEQ ID NO: 1819.
 XX Human; cytostatic; gene therapy; colon cancer; prostate cancer;
 KW breast cancer; lung cancer; cancer detection; ss.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200102568-A2.
 XX 11-JAN-2001.
 PF 30-JUN-2000; 2000WO-US18374.
 PR 02-JUL-1999; 99US-0142310.
 PR 02-JUL-1999; 99US-0142311.
 XX (CHIR) CHIRON CORP.
 PA (HYSE-) HYSEQ INC.
 XX Williams LT, Escobedo J, Innis MA, Garcia PD, Klinger J, Kassam A;
 PI Reuhard C, Randazzo F, Kennedy GC, Pot D, Lamson G, Drmanac R;
 PI Crkenjakov R, Drmanac S, Dickson M, Labat I, Leshkowitz D;
 PI Kita D, Garcia V, Jones LW, Strache-Crain B;
 XX WPI; 2001-091805/10.
 DR Library of polynucleotides for diagnosing a cancerous state of a
 XX mammalian cell and detecting cancer, particularly of the colon or
 PT prostate, comprises 3351 human polynucleotide sequences -
 XX Claim 9; Page 804; 1046pp; English.

XX WO200153312-A1.
 PN 26-JUL-2001.
 PD 26-DEC-2000; 2000WO-US34263.
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR P-PSDB; AAM40848.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Claim 1; SEQ ID NO 3993; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 1783 BP; 508 A; 383 C; 446 G; 446 T; 0 other;

Query Match 8.4%; Score 96.8; DB 22; Length 1783;
 Best Local Similarity 55.7%; Pred. No. 4.9e-14;
 Matches 185; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

QY 455 tgcgaccagtccgtggcagcactgcacccagcttcctcctggaaggccacatggaaatc 514
 DB 282 tcgcaccaggggggcgcacgccttgccaccatggcctcctggaaggccacatggagatg 341
 QY 515 ctggagaagcttcagataatggggccactgtggactccagatggctggactgcaca 574
 DB 342 gtcaattactctggccaaaggccaaatatacaatgattgcaagaagaccggcgt 401
 QY 575 gccatgcatggcctgcgcggggccacttagaggttgtaaaccttcgaaagccat 634
 DB 402 gctctgactgggcagcacaatggggccacttgatgtgtgactgtgtcattaacct 461
 QY 635 gagcagacacacaaatgtgaggataagctgtgagcaccacccctgcactggcagtcgg 694
 DB 462 ggccgagaagtgacctgtgaagataagaagggttataccctctgcatgctgcacctcc 521
 QY 695 acaggggcaggtgagatgttgagcacttctatccctggcctggcctggaatacgaatgcaga 754
 DB 522 aatggacagattaatgtttcagaagatcctcctgaacctgggggtggagattgatgaatc 581

QY 755 gacagggaaggagatactgacctgcctgcacgc 786
 DB 582 aatgtctatggaatacacagcgcttcacatgc 613

RESULT 8
 AAI58218
 ID AAI58218 standard; cDNA; 2894 BP.
 XX AAI58218;
 AC AAI58218;
 XX 22-OCT-2001 (first entry)
 DT Human polynucleotide SEQ ID NO 421.
 DE
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 XX Homo sapiens.
 OS WO200153312-A1.
 PN 26-JUL-2001.
 XX 26-DEC-2000; 2000WO-US34263.
 PF 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX (HYSE-) HYSEQ INC.
 XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX WPI: 2001-442253/47.
 DR P-PSDB; AAM39062.
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX Claim 1; SEQ ID NO 421; 10078pp; English.
 XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAI42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX Sequence 2894 BP; 808 A; 627 C; 741 G; 718 T; 0 other;

Query Match	8.4%;	Score 96.8;	DB 22;	Length 2894;
Best Local Similarity	55.7%;	Pred. NO. 5.7e-14;		
Matches 185;	Conservative 0;	Mismatches 147;	Indels 0;	Gaps
QY	455	tgcgacaggttcgctgcgacagcactgcacgcagcttccctggaagccacatggaatc	514	
Db	315	tccgaccgaggggcgacacgcttgaccatgcgctctgaacggccacgtgagatg	374	
QY	515	ctggagaagtcttagataaatggggccactgtggacttccaggatcggctggactgcaca	574	
Db	375	gtcaatttactcttggccaaaggggcaaatatcaatgcatttgacaagaaggaccgcgt	434	
QY	575	gccatgcattggcctgcgcggggccactttagagtggtgaaacttctcaaaagccat	634	
Db	435	gctctgactgggcagcatacataggccacttggatgtgttagcattgctcattaacat	494	
QY	635	ggagcagacaccaatgtgaggataagctgtgcagaccccgctgcagctggcagtc	694	
Db	495	ggcgagagtgacctgtaaggataagaagggtttataccccctctgcatgctgcagctcc	554	
QY	695	acagggcaggtggagattgtgagcactttctatccctgggctggaatacaatgccaga	754	
Db	555	aatgagcagattaatgtgttcgaagcatcctcgaacctgggggtggagattgatgaaatc	614	
QY	755	gacaggaaggggatactgcctctgcatagcgc	786	
Db	615	aatgtctatgaaatacagcgcttcacatcgc	646	
RESULT	9			
AAH57380				
ID	AAH57380	standard; cDNA; 7185 BP.		
AC	AAH57380;			
XX				
DT	10-SEP-2001	(first entry)		
XX				
DE	Human skeletal muscle cell specific cDNA sequence SEQ ID NO:220.			
XX				
KW	Human; tissue specific; diagnosis; brain; heart; skeletal muscle;			
KW	liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;			
KW	metabolic disease; developmental disease; cytostatic; immunomodulatory			
XX	neuroprotective; gene therapy; cancer; immunopathology; neuropathology			
OS	Homo sapiens.			
XX				
PN	WO200132927-A2.			
XX				
PD	10-MAY-2001.			
XX				
PF	02-NOV-2000; 2000WO-US30396.			
XX				
PR	04-NOV-1999; 99US-0163508.			
XX				
PA	(INCY-) INCYTE GENOMICS INC.			
XX				
PI	Sornasse T, Seilhamer JJ, Watson GA;			
XX				
DR	WPI; 2001-291057/30.			

their fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical agents. Expression of (I) in a sample indicates the differentiation of embryonic stem cells into a tissue selected from brain, heart, kidney, liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used to produce an expression profile that defines a metabolic or developmental process, treatment, condition, disease or disorder. The gene profile can be used for diagnosis, prognosis or monitoring of treatments and for investigating a predisposition to a disorder where the gene is associated with a cancer, immunopathology or neuropathology.

Query Match	7.5%	Score	86.6;	DB	22;	Length	7185;
Best Local Similarity	47.9%	Pred.	No. 2.le-11;				
Matches	282;	Conservative	0;	Mismatches	304;	Indels	3;
Gaps	1;						
Qy	299	aagaagcggagcgtctggccgctcgcatgacgccccagagccgagcgatcact	358				
Db	1724	aagtacgggaaggtgcgggtggcgagagctgctgtggagcgggacacacccgaaatgct	1793				
Qy	359	ggccctgtggaatgaggagacatctcctaaaaagctcggtggaggggaaaaatgaaggtcatt	418				
Db	1784	gccggaaaaatgccatgacccctcgacgtggcgtcccatcaacaacactggacatc	1843				
Qy	419	gagaagttcttgcctgac--gggggtcaaccacacagtcgacacagttccgtcgagaca	475				
Db	1844	gtcaagtgcgtctccccggggcgctccccgcacagccctgctggaaatggtctacacc	1903				
Qy	476	gcactgcaccgagcttccctgaagggcacatggaaatcctggagaagcttctagataat	535				
Db	1904	ctttgcaatcgtgccaaagcagaacagtgaggtggccgtagtctgctgcagtat	1963				
Qy	536	ggggccaactgtggacttccaggatcgccgtgactgcacagccatgcattgggctgcgcg	595				
Db	1964	gggggtcagcaaacgccagtcggtgcaaggtgtgacgcccttcaactggcgcccgag	2023				
Qy	596	ggggccacttagagtggtgaaactctcaaaagccatggacgagacacacaaatgtgag	655				
Db	2024	gagggccacgcagagatggtggctgctgctctcgaaacaaagccaatggcaacctgggg	2083				
Qy	656	gataagctgtgacaccccctgcacgtgcagctgcgcgacagggcgaggtggagatgtg	715				
Db	2084	aacaagcgactcaactccccctcatctgtgtagcaaaaggccacagttccagtgga	2143				
Qy	716	gagcaatttctatccctgggctggaataatcaatgccagagacaggggaagtactgccc	775				
Db	2144	gatgtctgatacaaacggtgtcatggtggacccacacccggatgggtacactccc	2203				
Qy	776	ctgcatgacgtgtgaggctcaacgcgtacaaaaatcatcaaacgtctgctcctgcattgg	835				
Db	2204	ctccatgtggccagtacctatggaacaatcaagctggggaagtcttctgctgcagcaccag	2263				
Qy	836	gctgacatgatacaagaacactggcaggaaagaccocgcagcgaactgg	884				
Db	2264	gcadagtccaatgcgaacacgaactagatatacagccccctgtgacacga	2312				

RESULT	10
AAC76497	
ID	AAC76497 standard; cDNA; 3040 BP.
XX	
XX	
AC	AAC76497;
XX	
XX	
DT	08-FEB-2001 (first entry)
XX	
DE	Human ORFX ORF2052 polynucleotide sequence SEQ ID NO:4103.
XX	
XX	
KW	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW	vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;

XX New cell and tissue specific polynucleotides useful for diagnosis, PT
PT prognosis or monitoring of treatments for disorders where the gene PT
PT associated with a cancer, immunopathology or neuropathology - XX
XX Claim 1; Page 148-150; 327pp; English.
XX
XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide
CC sequences (I). (I) can have cytostatic, immunomodulatory and CC
CC neuroprotective activities, and can be used in gene therapy. (I) and CC
CC proteins (II) encoded by then are used in high throughput screening CC
CC assays to select DNA molecules, RNA molecules, peptide nucleic acids, CC
CC mimetics, peptides, proteins, agonists, antagonists, antibodies or CC

KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive; ss.
XX
OS Homo sapiens.
XX
XX WO200058473-A2.
PN
XX
XX 05-OCT-2000.
PD
XX
XX 31-MAR-2000; 2000WO-US08621.
PF
XX
XX 31-MAR-1999; 99US-0127607.
PR
XX 02-APR-1999; 99US-0127636.
PR
XX 05-APR-1999; 99US-0127728.
PR
XX 30-MAR-2000; 2000US-0540763.
PR
XX
PA (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
PI
XX WPI; 2000-602362/57.
XX P-PSDB; AABA2288.
DR
XX
PT Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 3287-3289; 5507pp; English.
PS
XX
CC AAC74446 to AAC77606 encode the proteins given in ABA40237 to ABA43397,
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antisporadic; antiparkinsonian; nootropic; neuroprotective;
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC antithyroid; and antianaemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORFX-associated disorder. The
CC nucleic acids can be used to express ORFX proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 3040 BP; 680 A; 915 C; 934 G; 506 T; 5 other;

[illegible]

Qy	498	agggccacatggaatacctctggagagagcttctagataatg---gggccactgtgagacttcc	554
Db	1448	aaggccactacgaagtggtccagctactgctttcaaatggacggtgagcgtcaactgtc	1507
Qy	555	agatcggtgactgcacagccatgcattgggacctgcgcggggccacttagagtgg	614
Db	1508	agatgacggagggtggacaccatgatctgggccacagatgatacaagcacgtgacctcg	1567
Qy	615	tgaacttctgcaaacccatggagcagacacccaatgtgagggtataaagtctgtagcacc	674
Db	1568	tgaagctgctgtctccaaggctctgacatcaacatccgagacaacgaggagaacattt	1627
Qy	675	cgctgcacgtggcagtcgcgacaggcgaggtggagatgtgagcacctttctatccctgg	734
Db	1628	gctgcaactggggcggtctctcggctgctggtgacatgacgagatcctctggtctgcca	1687
Qy	735	gctggaataatccagacagacagggaagggtactgcctcatgacgctgtgaggc	794
Db	1688	agtgcgacctccacgcgtgaaactccacggagactgccactgcacatgccgcccggg	1747
Qy	795	tcaaccgctacaaaatcatcaaacctgctgctctctgctggtggctgacatgatgaccaaga	854
Db	1748	agaacgcgtacagctgtgcgtctctttcttcttcggtattcagatgcaccttaaga	1807
Qy	855	acctggcaggaagacccc	873
Db	1808	acaaggaggagagacgc	1826
RESULT 11			
AAH46914			
ID	AAH46914 standard; cDNA; 2348 BP.		
AC	XX		
AAH46914;	XX		
25-SEP-2001 (first entry)	XX		
cDNA encoding human protein kinase SGK288.			
Protein kinase; enzyme; cytostatic; nootropic; neurotropic; neuroprotective; human; antiparkinsonian; virucide; antibacterial; antifungal; antimigraine; analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic; antispasmodic; antirheumatic; antiarthritic; ophthalmologic; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropic; antidiabetic; gene therapy; ss.	XX		
Homo sapiens.	XX		
OS	XX		
Key	Location/Qualifiers		
CDS	54..2348		
FT	/*tag= a		
FT	XX		
XX	WO200155356-A2.		
XX	XX		
PD	02-AUG-2001.		
XX	XX		
PF	25-JAN-2001; 2001WO-US02337.		
XX	XX		
PR	25-JAN-2000; 2000US-0178078.		
PR	31-JAN-2000; 2000US-0179364.		
PR	17-FEB-2000; 2000US-0183173.		
PR	17-MAR-2000; 2000US-0190162.		
PR	29-MAR-2000; 2000US-0193404.		
PR	13-NOV-2000; 2000US-0247013.		
XX	(SUGE-) SUGEN INC.		
XX	XX		
PI	Plowman G, Whyte D, Manning G, Sudarsanam S, Martinez R;		
XX	XX		
DR	WPI; 2001-476202/51.		
DR	P-PSDB; AAB85514.		
XX	XX		


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Db 656 acgaggtcagctcgcgcgcacccctagactccctgtccatccacagctcgagcac 715
Qy 495 tggagccacatgaaatcctcgtgagagctctctagataatggggccactgtgacttcc 554
Db 716 agggggagctggaccagctgaaggagcatttgcggaaagtgcacactcgtccacaaagc 775
Qy 555 aggatcggctggactgcacagccatgctatgggctcgcgcggggccacttagagtg 614
Db 776 cagacgagcgcgcttcaccccccctcctggtcgcctcgccttggagagattgagaccg 835
Qy 615 tgaacttcgcaagccatgagcagacacccaatgtgaggataagctgctgagacccc 674
Db 836 ttgcctcctcgtgagtggtggtgcgcaccccccacactcctggcaaaagagcgagagcg 895
Qy 675 cgtcgcagctggcagctgcgcagcagcaggtggagattgtgagcactttctatccctgg 734
Db 896 cctcgtcgtgcgcacagcgcgtcacagacattgtgggctgctgctgagagcgtg 955
Qy 735 gctcggaaataatcgcagagacagggaggggatactgcctgcagcagcgtgagggc 794
Db 956 acgtggacatacaatctatgtatggagcctgtggtcgcggcggcgtgacactcaccacgaag 1015
Qy 795 tcaaccgctacaaaatcataaactgctcctcgtcgtgagggcagcagcactgtgtacgtgtgcgcg 1015
Db 1016 ggaaccacgtgaaatgcgttgagcctgtggtcgcggcggcgtgacactcaccacgaag 1075
Qy 855 acctggcaggaagaccccccgcgcagcctgg 884
Db 1076 ccgactcgtgcacaccccgatgaccttg 1105

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RESULT 14

AAV38678
ID AAV38678 standard; DNA; 2649 BP.

XX AC AAV38678;

XX DT 27-OCT-1998 (first entry)

XX DE Mus musculus SOCS10 gene.

XX KW SOCS; suppressor of cytokine signalling; PCR primer;
XX KW autoimmune disease; diagnosis; cancer; treatment;
XX KW cytokine mediated cellular responsiveness; hyperimmunity;
XX KW immunosuppression; allergies; hypertension; ss.

XX DS Mus musculus.

XX PN W09820023-A1.

XX PD 14-MAY-1998.

XX PF 31-OCT-1997; 97WO-AU00729.

XX PR 14-FEB-1997; 97AU-0005117.

XX PR 01-NOV-1996; 96AU-0003384.

XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.

XX PI Alexander WS, Hilton DJ, Metcalf D, Nicholson SE;

XX PI Nicola NA, Richardson RT, Starf R, Viney EM, Willson TA;

XX DR WPI; 1998-286854/25.

XX PT Suppressor of cytokine signalling proteins - useful to treat
XX PT disease, injury or abnormality involving cytokine mediated cellular
XX PT responsiveness e.g. hyperimmunity, immunosuppression, allergies and
XX PT hypertension

XX PS Claim 14; Page 153-155; 325pp; English.

XX CC The sequence is that of a gene encoding a suppressor of cytokine

CC signalling protein (SOCS). SOCS can be used to screen for naturally
CC occurring antibodies to SOCS, which may occur, e.g. in some autoimmune
CC diseases. Alternatively, specific antibodies can be used to
CC screen for SOCS, which is useful as a knowledge of SOCS levels
CC may be important for the diagnosis of certain cancers. Soluble
CC SOCS polypeptides can be used to treat disease, injury or
CC abnormality involving cytokine mediated cellular responsiveness,
CC e.g. hyperimmunity, immunosuppression, allergies and hypertension.
XX XX

SQ Sequence 2649 BP; 559 A; 791 C; 749 G; 550 T; 0 other;

Query Match 6.7%; Score 77.2; DB 19; Length 2649;

Best Local Similarity 48.4%; Pred. No. 2.9e-09;

Matches 214; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

```

Qy 386 aaagctcgggtggagggaataaaggtcattgagagattcctggctgacgggggtca 445
Db 619 aaagcctgtgagcgcaagaacgcggagcgtgaggaattatggcgatacaacgcagac 678
Qy 446 gccgacacgtgcgaccagttccgtcggacagcactgcaccgagcttccctggaagggcac 505
Db 679 gccaacaccgctgtaacagggcgtggaccgcactgcacgagctgtctccgcaatgac 738
Qy 506 atgaaatcctcggagaagctctctagataatggggccactgtggaactccagatcgctg 565
Db 739 ctggaggtcatggagactcctagtagtgcgggggccaaagtggaaggcaagaatgtctac 798
Qy 566 gactgcacagccatgcattggcctgcgcggggggccacttagagtggtgaaactctg 625
Db 799 agcatcaccccttctgttggctgcccagagtgggcagctggagggcctgaggtctctg 858
Qy 626 caaagccaatgagcagacacccaatgtgagggataagctgtgagcaccctcgtgcacgtg 685
Db 859 gccaaagcatgtgcagacatcaacacgcagccagtcagtcagtcagccctctacagag 918
Qy 686 gcagtccggcagcagggcaggtggagattgtgagcacttctctcctcctggcctggaatc 745
Db 919 gccagcaagaatgagcatgaagacgtgtagagttctctctcctcagggcgccgagct 978
Qy 746 aatgccagagacagggaggagatactcctcctgcagcagctgtgagctcaaccgctac 805
Db 979 acaaaagccaacaggcgcgtcctccctcctgcatgttgcctccaagagggaactat 1038
Qy 806 aaatcatcaaaactgctgctcc 827
Db 1039 agaatagtgcagatgctgtgc 1060

```

RESULT 15

AAF83200
ID AAF83200 standard; DNA; 3454 BP.

XX AC AAF83200;

XX DT 09-JUL-2001 (first entry)

XX DE Human kidney ankyrin G119 (AnkG119) protein encoding DNA.

XX KW Ankyrin G119; AnkG119; kidney; human; spectrin binding domain;
XX KW regulatory domain; integral membrane protein; secretory protein; ds.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 131..3397

XX FT FT /*tag= a

XX FT FT /*product= "AnkG119"

XX PN US6225086-B1.

XX PD 01-MAY-2001.

XX XX

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PF 21-MAY-1998; 98US-0082059.
XX
PR 21-MAY-1997; 97US-0047356.
XX
PA (UYUA ) UNIV YALE.
XX
PI MORROW JS, Devarajan P;
XX
DR WPI; 2001-315683/33.
XX
DR P-PSDB; AAB62429.
XX
PT Novel isolated nucleic acid encoding ankyrin G119 protein, useful for
PT producing recombinant ankyrin G119 protein which participates in
PT trafficking of secretory proteins between endoplasmic reticulum and
PT compartments
XX
XX
PS Claim 4; Fig 2A-C; 40pp; English.
XX
XX
CC The invention relates to a human ankyrin G119 (AnkG119) protein. The
CC AnkG119 has a molecular weight of 116 kDa and comprises a region
CC consisting of 13 repeats of a 33 residue structure and further comprises
CC a spectrin binding domain and 5 kDa regulatory domain. The AnkG119
CC nucleic acid is useful for producing the protein by standard recombinant
CC techniques. The AnkG119 protein participates in the trafficking of
CC integral membrane proteins and secretory proteins between the endoplasmic
CC reticulum and other membrane compartments. The present sequence
CC represents the DNA encoding the human kidney Ankg119 protein.
XX
XX
SQ Sequence 3454 BP; 1043 A; 802 C; 797 G; 812 T; 0 other;

Query Match 6.5%; Score 75.6; DB 22; Length 3454;
Best Local Similarity 47.5%; Pred. NO. 7.7e-09;
Matches 225; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 378 cttctgaaagctgcggtgaggaggaataaaggtcattgagaagttcctggctgacg 437
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 993 ccgtccatctcagctcagggaaggagcggtggacatggtcgtcgtctcctcgtagaa 1052
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 438 gggggtcagccgacgtgcgaccagttccgtcgcagacagcactgcacgagcttccctgg 497
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1053 atgcgaatgtgaacctgagcaataagagcggcctgacccactcatttggctgtcaag 1112
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 498 aaggccacatgaaatcctcggagagctctctagataatggggccactgtggactccagg 557
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1113 aagatcgagtgaatgtggcagaagtcctcgttaacacaaagggctcatgtggacgccaga 1172
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 558 atcggctgactgcacagcattggtggtggtggtggtggtggtggtggtggtggtggtg 617
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1173 caaagatggatacacaccactgcatgtgggctgacctatggaatatcaagattgtta 1232
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 618 aacttctgaaagccatggagcagacacaaatgtgaggataagctgctgagcaccgcg 677
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1233 atttctgtccagcattctcgaagttaatgccaaacaaagatgggtatagccat 1292
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 678 tgcagctggcagtcggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 737
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1293 tacatcaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1352
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 738 tggaaatcaatgccagagacagcagcagcagcagcagcagcagcagcagcagcagcagc 797
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1353 cctccccaatgaactcactgtgaatgggaatactgaccttggcattgcccggtgctcg 1412
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 798 accgtcaaaaatcatcaactgtctcctgcatggggctgacatgaccca 851
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1413 gctacatctcagtagtgacacccctgaagatagtagccgaagaacacatgaccca 1466
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Search completed: April 17, 2002, 09:31:29
Job time: 4933 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 17, 2002, 08:09:16 ; Search time 1550.75 Seconds
(without alignments)
8024.254 Million cell updates/sec

Title: US-09-758-593A-2

Perfect score: 1158

Sequence: 1 cagctcgaggacgcacca.....ctaccacaataaaaagctg 1158

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

arched: 11351937 seqs, 5372889281 residues

total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- EST:*
- 1: em_estfun:*
 - 2: em_esthum:*
 - 3: em_estin:*
 - 4: em_estom:*
 - 5: em_estpl:*
 - 6: em_estba:*
 - 7: em_estro:*
 - 8: em_estov:*
 - 9: em_htc:*
 - 10: gb_est1:*
 - 11: gb_est2:*
 - 12: gb_htc:*
 - 13: gb_gss:*
 - 14: em_gss_fun:*
 - 15: em_gss_hum:*
 - 16: em_gss_inv:*
 - 17: em_gss_pln:*
 - 18: em_gss_pro:*
 - 19: em_gss_rod:*
 - 20: em_gss_vrt:*
 - 21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568.4	49.1	749	11 BF790486	BF790486 602250156
2	548.6	47.4	610	10 AW044467	AW044467 wx22c10.x
3	530.2	45.8	875	11 B1413513	B1413513 602987535
4	492.4	42.5	504	11 BE926721	BE926721 QV2-BN063
5	433.4	37.4	456	10 AJ346356	AJ346356 SHR-00001
6	423.8	36.6	435	11 F24585	F24585 HSPD11011 H
7	420.4	36.3	567	11 BF189893	BF189893 235854 MA
8	415	35.8	417	11 F32675	F32675 HSPD25601 H
9	410.2	35.4	457	11 F36391	F36391 HSPD33981 H
10	402	34.7	408	10 AJ346328	AJ346328 SHR-00001
11	399.2	34.5	423	10 AJ346414	AJ346414 SHR-00001
12	393.6	34.0	537	11 BF189892	BF189892 235852 MA

13	390.4	33.7	504	11 BE809163	BE809163 214554 MA
14	384.4	33.2	412	10 AJ346604	AJ346604 SHR-00001
15	383.2	33.1	489	11 BF775625	BF775625 285833 MA
16	382	33.0	408	10 AA180314	AA180314 ZP34902.S
17	379.4	32.8	385	11 F25326	F25326 HSPD12307 H
18	369.4	31.9	380	11 F28193	F28193 HSPD16804 H
19	366.2	31.6	371	10 AJ346337	AJ346337 SHR-00001
20	354	30.6	372	10 AJ346193	AJ346193 SHR-00001
21	352.4	30.4	354	10 AJ346514	AJ346514 SHR-00001
22	348	30.1	350	11 F28615	F28615 HSPD17872 H
23	348	30.1	360	11 F28533	F28533 HSPD17696 H
24	323	27.9	324	11 F24152	F24152 HSPD10215 H
25	318	27.5	341	11 F19619	F19619 HSPD04224 H
26	314	27.1	326	10 AW237359	AW237359 xm70f06.x
27	307.4	26.5	325	10 AJ346541	AJ346541 SHR-00001
28	307	26.5	321	10 AJ346516	AJ346516 SHR-00001
29	306.8	26.5	391	11 BF599511	BF599511 263321 MA
30	299	25.8	302	10 AJ346216	AJ346216 SHR-00001
31	299	25.8	321	10 AJ345979	AJ345979 SHR-00001
32	297	25.6	299	10 AJ346507	AJ346507 SHR-00001
33	297	25.6	299	10 AJ346764	AJ346764 SHR-00001
34	297	25.6	301	10 AJ346249	AJ346249 SHR-00001
35	297	25.6	308	10 AJ346729	AJ346729 SHR-00001
36	297	25.6	308	10 AJ346755	AJ346755 SHR-00001
37	297	25.6	309	10 AJ346346	AJ346346 SHR-00001
38	297	25.6	310	10 AJ346006	AJ346006 SHR-00001
39	297	25.6	311	10 AJ346355	AJ346355 SHR-00001
40	297	25.6	315	10 AJ346055	AJ346055 SHR-00001
41	297	25.6	321	10 AJ345972	AJ345972 SHR-00001
42	296	25.6	312	11 F29659	F29659 HSPD19655 H
43	295.4	25.5	302	10 AJ346566	AJ346566 SHR-00001
44	295.4	25.5	311	10 AJ346339	AJ346339 SHR-00001
45	295.4	25.5	314	10 AJ346191	AJ346191 SHR-00001

ALIGNMENTS

RESULT 1

LOCUS BF790486 749 bp mRNA 12-JAN-2001

DEFINITION 602250156F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4337892 5', mRNA sequence.

ACCESSION BF790486

VERSION BF790486.1 GI:12095536

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 749)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLOM1212 row: 0 column: 13
High quality sequence stop: 649.
Location/Qualifiers
1. 749
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4337892"
/clone_lib="NIH_MGC_81"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB"

FEATURES
source

M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

COMMENT

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=6t2-QV2-BT0634-280
800-331-b12&t3=2000-08-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 504.

FEATURES

1. .504
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0634"
/dev_stage="Adult"

/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196 /716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 114 a 147 c 158 g 85 t

ORIGIN

Query Match 42.5%; Score 492.4; DB 11; Length 504;
Best Local Similarity 99.8%; Pred. No. 2.2e-100;
Matches 493; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 555 agatcgctgactgcagcagcattgagcctgcgcggggccacttagagtg 614
DB 11 AGGATCGGTGACTGCACAGCCATGCAATGGCCCTGCCGGGGCCACTTAGAGGTGG 70
QY 615 tgaacctctgcaaaagccatgagcagacaccaatgtgaggataagctgctgagcaccc 674
DB 71 TGAACCTTCTGCAAGCCATGGAGCAGACACCAATGTGAGGATAGCTGTGAGCACCC 130
QY 675 cgctgcactggcagtcgccgacagggcaggtgagattgtgagcaactttctacctgg 734
DB 131 CGCTGCACGTGGCAGTCCGGACAGGGCAGGTGGAGATTGTGGATCACTTTCTATCCCTGG 190
QY 735 gcttggaaatcaatgccagagacaggaagggtactcctcgatgcgtgtagcg 794
DB 191 GCCTGGAATCAATGCCAGACAGGGAAGGGGATACTGCCCTGATGACGCTGTGAGGC 250
QY 795 tcaaccgctacaaaatcatcaaaactgctcctcgatggggtgacatgatgacaaaga 854
DB 251 TCAACCGCTACAAAATCATCAAACTGCTCCTGCATGGGCTGACATGATGACCAAGA 310
QY 855 acctggcagaaagaccccgacggacctggtcagctctggcaggtgatataccggcacg 914
DB 311 ACTTGGCAGGAAGACCCCGACCGACCTGGTGCAGCTCTGGCAGGCTGATACCCGSCAG 370
QY 915 ccttgagcatctgagcgggggtgagcataaaggcgtgagggcctaatgatagtg 974
DB 371 CCTTGGAGCATCTTGAGCCGGGGGTGACATACGGGGCTGAGGGGCCCTAATGATG 430
QY 975 ggcgagagacccctcagcctgtgcccagccagtgatgcgtgcccccagccagccagctta 1034
DB 431 GCGCAGAGAGCCCTCAGCCCTGTGCCAGCCAGTGAATGCTGCCCCAGCCAGCCAGCTA 490

QY 1035 ccagcccccctctct 1048
DB 491 CCAGCCCTCTCT 504

RESULT 5

AJ346356 456 bp mRNA EST 14-AUG-2001
DEFINITION SH-000016-0-I21 HM3/S3 Homo sapiens cDNA, mRNA sequence.
ACCESSION AJ346356
VERSION AJ346356.1 GI:15167539
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 456)
Laveder,P., De Pitta,C., Toppo,S., Valle,G. and Lanfranchi,G.
Specific subtraction of abundant mRNAs in skeletal muscle
Unpublished (2001)
JOURNAL CONTACT: Laveder P
COMMENT CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy

FEATURES

1. .456
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: p0PD (Custom); Site_1: EcoRI; Site_2: NotI;
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"

BASE COUNT

119 a 132 c 126 g 79 t

ORIGIN

Query Match 37.4%; Score 433.4; DB 10; Length 456;
Best Local Similarity 99.8%; Pred. No. 3.6e-87;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 724 tctatccctggcctggaaatcaatgccagacaggaagggtactgcccctcatga 783
DB 1 TCTATGCCCTGGCCCTGGAAATCAATGCCAGACAGGGAAGGGGATACGCCCTGCATGA 60
QY 784 cgctgtgaggtcacaacccgctacaaaatcatcaaaactgctcctcgatggggtgacct 843
DB 61 CGCTGTGAGGCTCAACCGCTCAAAATCATCAAACTGCTGCTCCTGCATGGGCTGACAT 120
QY 844 ggtaccacgaacacctggcaggaagacccccgcagcctggtgcagctctggcaggtga 903
DB 121 GATGACCAAGAACCTGGCAGGAAGAACCCCGACCGACCTGTGTGACGTGTGCGAGCTGA 180
QY 904 taccgcgcacgcctggagcatcctgacgggggctgagcataaaggctgaggggcc 963
DB 181 TACCCGGGCACGCCCTGGAGCATCTCTGAGCCGGGGGCTGAGCATACGGGCTGGAGGGGCC 240
QY 964 taatgatagtggcgagagacccctcagcctgtgcagccccagtgaatgcgtgcccccagc 1023
DB 241 TAATGATAGTGGCGAGAGACCCCTCAGCCTGTGCGACGCCAGTGAATGCGTGCCCCAGC 300
QY 1024 ccagccagctaccacgcccctctctgtgagccggaggggtctctaaagaatggtccocgg 1083
DB 301 CCAGCCAGCTACCCAGCCCTCTCTGTGTGTCAGCCGGAGGGTCTTAAGAAATGGCTCCCGG 360
QY 1084 agctaacctgagggccagccctttttctgcatgattccagagacacataccacaaactacc 1143

/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pcDNAII (Invitrogen); Site.1: BstXI;
Site.2: NotI; The library was constructed by G.
Lanfranchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
oligo-dT-NotI primer
(5'-biotin-AACCGGCTCGAGCGCGCTTTT-3'). The
ds cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pcDNAII vector."
BASE COUNT 121 a 128 c 126 g 79 t 3 others
ORIGIN

Query Match 35.4%; Score 410.2; DB 11; Length 457;
Best Local Similarity 98.8%; Pred. No. 5.8e-82;
Matches 412; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 741 aaatcaatgcagagacaggaagggtactgcccctgcacgactgtgaagctcaacc 800
Db 1 AAATCAATGCCAGACAGAGAGGGGATACGCTCCTGCATGACCTGTGAGGCTCAACC 60
Qy 801 gctcaaaatcaatcaactgtctcctcgtcatggggctgacatgatgaccagaacctgg 860
Db 61 GCTGAAAAATCATCAATGCTGCTCCTGTCATGGGCTGACATGATGACCAAGAACCTGG 120
Qy 861 caggaaagacccccagacgactgtgtgagctctgagcgtgatacccgcaacccctgg 920
Db 121 CAGGAAAGACCCCGACGACCTGTGTGAGCTGTGACAGGCTGATACCCGGCACGCCCTGG 180
Qy 921 agcatcctgagccggggctgagcataacggctgagggcctaatatgtagtggcag 980
Db 181 AGCATCTTGACCGGGGCTGAGCATACGGCTGGAGGGGCTTAATGATGGGCCAG 240
Qy 981 agaccctcagcctgtgcccagccagtgatgctgccccagccagccagctaccagc 1040
Db 241 AGACCCCTCAGCCTGTGCGCAGCCAGTCAATGCTGCGTCCCGCCAGCCAGCTACCCAGC 300
Qy 1041 cccctctgtgtgagccggaggtctcctaagaatggtccccggagcactgagggccca 1100
Db 301 CCCCTCTGTGTGAGCGCGAGGGTCTTAAGAAATGGCTCCCGAGCTAACTGAGGGGCCCA 360
Qy 1101 gcctttttctgcatgattccaggagcacataccacaactaccacaataaaaaagct 1157
Db 361 GCCTTTTCTGCTATGATCCAGGAGCACATACCACANACTACCANCAATAAAAAAGCT 417

RESULT 10
AJ346328 408 bp mRNA EST 14-AUG-2001
LOCUS
DEFINITION SHR-000016-0-H10 HM3/S3 Homo sapiens cDNA, mRNA sequence.
ACCESSION AJ346328
VERSION AJ346328.1 GI:15167511
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 408)
AUTHORS Laveder, P., De Pitta, C., Toppo, S., Valle, G. and Lanfranchi, G.
TITLE Specific subtraction of abundant mRNAs in skeletal muscle
JOURNAL Unpublished (2001)
COMMENT Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50393
ABI Chromatograms and other information are available on WWW at
http://muscle.cribi.unipd.it
Seq primer: PC2R.

FEATURES
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/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (Custom); Site.1: EcoRI; Site.2: NotI;
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"
BASE COUNT 99 a 125 c 118 g 66 t
ORIGIN

Query Match 34.7%; Score 402; DB 10; Length 408;
Best Local Similarity 100.0%; Pred. No. 3.9e-80;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 757 cagggaagggtactgcccctgcacgactgtgaggtcaaccgctacaataatcaaa 816
Db 7 CAGGGAAGGGGATACGCTCCTGCATGACCTGTGAGGCTCAACCGCTACAAATCATCAA 66
Qy 817 actgtctcctcgtcatggggctgacatgatgaccagaacctggcaggaagaccctgac 876
Db 67 ACTGTGCTCTCTGTCATGGGGCTGACATGATGACCAAGAACCTGGCAGGAAGACCCGAC 126
Qy 877 ggaacctgtgagctctgagcagctgatacccgcaacgccccctggagcactcctgagccggg 936
Db 127 GGACCTGTGTGACAGCTGTGGCAGGCTGATACCCGGCACGCCCTGGAGCATCTCTGAGCCGG 186
Qy 937 ggtcagcataacggctgaggggcccctaatgtagtgaggcgagagacccctcagcctgt 996
Db 187 GCTGAGCATACGGGCTGGAGGGGCTTAATGATGAGCGGAGAGACCCCTCAGGCTGT 246
Qy 997 gccagccagtgatgctgccccagccagccagctaccagccagccctcctctgtgtgcag 1056
Db 247 GCCAGCCAGTGAATGCTGTGCCCGCCAGCCAGCCAGCTACCCAGCCCTCTCTGTGTGCAG 306
Qy 1057 ccggaggtcctaaatggtctccggagcactgagggccagccagcctttttctgcatg 1116
Db 307 CCGGAGGGTCTTAAGAAATGGCTCCCGAGCTAACTGAGGGCCCGAGCCTTTTCTGTCATG 366
Qy 1117 atccaggagcacataccacaactaccacaataaaaaagctg 1158
Db 367 ATCCAGGAGCACATACCACAAATACCACATAAAAAAAGCTG 408

RESULT 11
AJ346414 423 bp mRNA EST 14-AUG-2001
LOCUS
DEFINITION SHR-000016-0-M09 HM3/S3 Homo sapiens cDNA, mRNA sequence.
ACCESSION AJ346414
VERSION AJ346414.1 GI:15167597
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 423)
AUTHORS Laveder, P., De Pitta, C., Toppo, S., Valle, G. and Lanfranchi, G.
TITLE Specific subtraction of abundant mRNAs in skeletal muscle
JOURNAL Unpublished (2001)
COMMENT Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50512
ABI Chromatograms and other information are available on WWW at
http://muscle.cribi.unipd.it
Seq primer: PC2R.
FEATURES
source Location/Qualifiers
1. 423

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/notes="Vector: pOPD (Custom); Site_1: EcoRI; Site_2: NotI;
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"
BASE COUNT 106 a 125 c 120 g 72 t
ORIGIN

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Query Match 34.5%; Score 399.2; DB 10; Length 423;
Best Local Similarity 99.3%; Pred. No. 1.7e-79;
Matches 401; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 755 gacagggaaggagatacctcctgcatgacgtgtgagctcaacgcgtacaaaatcattc 814
DB 1 GACTGGGAAGGGGATACTCCCTGTCATGACGCTGTGAGGCTCAACCGCTACAAAATCATC 60

QY 815 aaactgtctctcgtcgtgagctgacatgacacaaacacgtgcagaaagaccgcg 874
DB 61 AACTGCTGCTCTGCTGAGGCTGACATGCTGACCAAGAACTGCGAGAAAGACCCCG 120

QY 875 acggacctgtgctgagctgtgaggtgtatcccgccagccctgagcatccttgagccg 934
DB 121 ACGGACCTGTGTCAGCTCTGGCAGGCTGATACCGGCACGCCCTGTGAGCATCCTGAGCCG 180

QY 935 ggggtgacataaacgggtgagggcctaataatgtagtgggcagagagacccctcagcct 994
DB 181 GGGGCTGAGCATAAACGGGCTGAGGGGCTTAATGATGAGTGGCGAGAGACCCCTCAGCCT 240

QY 995 gtgcagccagtgatgagtgccagccagccagccagctaccagccctctctgtgtgc 1054
DB 241 GTGCCAGCCAGTGAATGCTGTCGCCAGCCAGCCAGCTACCCAGCCCTCTCTGTGTGC 300

QY 1055 agccggagggtcctaagaatgctcccgagctaaactgagggccagcctttttttgtgca 1114
DB 301 AGCCGGAGGGTCTTAAGAAATGGCTCCCGGAGCTAACTAGGCGCCAGCCAGCTTTTCTGCA 360

QY 1115 tgatccagagcacataccacaaactaccacataaaaaagctg 1158
DB 361 TGATCCAGGAGCAGATACCACAAACTACCACATAAAGAGCTG 404

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RESULT 12
LOCUS BF189892 537 bp mRNA EST 02-NOV-2000
DEFINITION 235852 MARC 2P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BF189892
VERSION BF189892.1 GI:11073333
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keale,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel.: 402 762 4366
Fax: 402 762 4390
Email: smiththemal.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.

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PCR Primers
FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTCAGTCACGAGG
Plate: 59 row: G column: 19
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. 537
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 2P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/notes="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
library made from pooled tissue from testis, ovary,
endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT 115 a 149 c 186 g 87 t
ORIGIN

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Query Match 34.0%; Score 393.6; DB 11; Length 537;
Best Local Similarity 90.5%; Pred. No. 3.1e-78;
Matches 420; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 356 actggccctgtgtaggagacacctctcctgaaagctgcgtgaggggaaatgaaggtc 415
DB 74 ACCGGCCCTGTGACGAGGAGACATTCCTGAAAGCGCGGTGGAGGGGAAATGAAGGTC 133

QY 416 attgagaattcctgctgacgggggtcagccgacacgtgcacagctccgtcgaca 475
DB 134 ATTGAGAAGTTCTGCGGATGGGGTTCCCGACACACCTCGACAGTTCCCGCCGACA 193

QY 476 gcactgcacccagctcctcctggaaggccacatggaaatccttgagaagctctctagataat 535
DB 194 GCCTTGACACGGCTTCCTTGAGGGCCACATGGAGATCCTGGAGAAGCTTCTGGAGAGT 253

QY 536 gggggcaactgtggaactccaggtgcgtgactgcacagccatgcattggccctgcgc 595
DB 254 GGGGCTACTGTGGAGTTCAGGATCGGTGGACTGCACAGCCATGCATTTGGCCTGCCGT 313

QY 596 gggggcaactgtgaggtgtgaaactctgcaagccatctggaagccatggagcagaccatgtgag 655
DB 314 GGGGCCACTTGGAGTGTGAAATCTCTGCAAGCCGAGGAGGACAGACACAGTGTGAGA 373

QY 656 gataagctgtgagcaccgccgtgcacgtggcagctccgacagggcgaggtggagattgtg 715
DB 374 GATAAGCTGCTGAGCACCCCACTGCACGTGGCGTCCGACGGGCACGCTGGAGATCGTG 433

QY 716 gagaactttctatccctgggctggaatcaatgcagagagagaggggatactgc 775
DB 434 GAACATTTTCTGCTGCGCTGGGCTGGACATCAATGCCAAAGACAGAGAGGGGACAGCGCC 493

QY 776 ctgcagctgtgaggtgacccgtcaaccgtcaaaaatcatcaaat 819
DB 494 CTGCAGGAGCGCTGAGACTCAACCGCTACAAAATCATCAAACT 537

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RESULT 13
LOCUS BE809163 504 bp mRNA EST 25-APR-2001
DEFINITION 214554 MARC 2BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BE809163
VERSION BE809163.1 GI:10240275
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 504)
Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-Mckown,C.G.,
Perteau,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and

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TITLE
JOURNAL
MEDLINE
COMMENT

Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
21180013
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCTCCAGTCAGCAGC
Plate: 71 row: G column: 3
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1. 504
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 2BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from testis, thymus,
semitendinosus muscle, longissimus muscle, pancreas,
adrenal, and endometrium."
BASE COUNT 129 a 127 c 169 g 79 t
ORIGIN

Query Match 33.7%; Score 390.4; DB 11; Length 504;
Best Local Similarity 85.9%; Pred. No. 1.6e-77;
Matches 433; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

Qy 15 gcaccatgagagactccgagcggtgcaagagggccacagcgctcatcgagcagcgctgg 74
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 GCACAATGCGAGACTCTGAGGAGGTGACGGGGCCACGGCACTTATTGAGGAGCGGCTGG 60

Qy 75 cacaggagagaggaatgagaaatcccgagagagacacgcgcgaagctgcccattggact 134
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 CACAGGAGGAGGAATGAGAACTCCGAGGAACCCACCATCAGAAGTTGCCCATGGAGA 120

Qy 135 tctgtgtctgagagatgagaagcaccagcggtgctcagagtgcagccctgcagaaggtga 194
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 TcTGTGTGTGAGGATGAGAAGCACCATATAGGCTTGAGAGTCCGTCCTTACAAAAGGTTA 180

Qy 195 agggccaagagcgctgcgaagacgctccctggacctgcgcgaggagatcctgatgtgg 254
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 AGGGCCAGAGCGCGTGGGAAGACATCTTAGACTCTCGGAGGAGAGATCATCGAGTGG 240

Qy 255 gcgggatccagaacctcatcagctgcggaagaaacgcgaagcagaagaagcgagcgctc 314
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GCGGATCCAGAACCTCATCCAGCTGCGGAAAAAAGCAAGCAGAAGAAACGGAAGCCC 300

Qy 315 tggccctctcgtatgagcgcgccccagagcccgagagagatacactggccctgtgatgag 374
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGGCGGCTCCAGAGGACCATCTCCAGAGCCAGAGGAGATTACGGGGCCCTGTGGACGAGG 360

Qy 375 agacctctctgaagctcggtggaggggaaaaatgaagctattgagaagttcctggctg 434
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 AGACATTCCTGNAAGCTCGGTGGAGGGGAGAGATGAAGGTCTATCAGAAAGTTTCTGGCGG 420

Qy 435 acgggggtctcagcgcagacgtgcgaccagttccgtcggacagcactgcaccagagcttccc 494
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ATGGGGGTTCCTCCCTCACACCTGTGATCAGTTTCGCGCGACTGCCCTGCACCGAGCTCCC 480

Qy 495 tggaaaggccacatggaatcctgg 518
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 TGGAGGGCCACATGGAGATCCTTG 504

RESULT 14

AJ346604
LOCUS AJ346604 412 bp mRNA EST 14-AUG-2001
DEFINITION SHF-000017-0-115 HM3/S3 Homo sapiens cDNA, mRNA sequence.
ACCESSION AJ346604
VERSION AJ346604.1 GI:15167787
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 412)
AUTHORS Laveder,P., De Pitta,C., Toppo,S., Valle,G. and Lanfranchi,G.
TITLE Specific subtraction of abundant mRNAs in skeletal muscle
JOURNAL Unpublished (2001)
COMMENT Contact: Laveder P
CRIBI Biotechnology Centre
University of Padua
Via U. Bassi 58/B, 35121 Padua, Italy
sequencing centre identifier: HSPD50806
ABI Chromatograms and other information are available on WWW at
http://muscle.cribi.unipd.it
Seq primer: PC2R.
Location/Qualifiers
1. 412
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HM3/S3"
/sex="female"
/tissue_type="pectoral muscle (after mastectomy)"
/note="Vector: pOPD (Custom); Site_1: EcoRI; Site_2: NotI;
caucasian; Skeletal muscle cDNA was depleted of hundred
most expressed mRNAs through an original two steps
subtractive procedure"
BASE COUNT 98 a 124 c 118 g 71 t 1 others
ORIGIN

Query Match 33.2%; Score 384.4; DB 10; Length 412;
Best Local Similarity 97.8%; Pred. No. 3.5e-76;
Matches 400; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

Qy 750 ccagagacaggaagggatactgcccctgcatgagctgagctgagctcaaccgctacaaa 809
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CCAGAGNCAGGAAGGGGAT--CTGCCCTGATGACGCTGTGAGGCTCAACCGCTACAAA 58

Qy 810 tcatcaaaactgtctctctgcatggggctgacatgatgaccaagaacctggcaggaaaga 869
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 TCATCAAACTGCTGCTCTGCTGTCATGGGGCTGACATGATGACCAAGAACCTTGGCAGGAAAGA 118

Qy 870 ccccgacgagacctgtgacgtctgtggcagctgatacccgccacgccctggagcatcctg 929
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 CCCCAGCAGGACCTGTGTGACGCTGTGGCAGGCTATACCCGGCAGCCCTTGGAGCATCTCG 178

Qy 930 agccgggggctgagcataacggctggaggcctaatgatagtggcgagagacccctc 989
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 AGCCGGGGCTGAGCATACGGGGCTGGAGGGGCTTAATGATAGTGGCCGAGACACCCCTC 238

Qy 990 agcctgtgcccagcccagtgaaatgcgtgccccagccagccagctaccagcccccctctg 1049
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 AGCCTGTGCGACCCAGTGAATGCTGTCGCCACGCCAGCCAGCTACCCAGCCCTCTCTG 298

Qy 1050 tgtcagccggagggtccttaagaatggctcccgaggactaactgagggccagcccttttt 1109
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 299 TGTGACGCGGAGGGTCTTAAGAATGGCTCCGGAGCTAACTGAGGGCCAGCCTTTTTT 358

Qy 1110 ctgcatgatccagagacacataccacaaactaccacaaataaaaaaactg 1158
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 CTGCATGATCCAGGAGCACATACCACAAACTACCACATAAAAAAGCTG 407

RESULT 15
BF775625

BF775625	BF775625	489 bp	mrna	EST	25-APR-2001
LOCUS	285833	MARC 3BOV Bos	taurinus	cdNA 5', mRNA sequence.	
DEFINITION	BF775625				
ACCESSION	BF775625				
VERSION	BF775625.1	GI:12123525			
KEYWORDS	EST.				
SOURCE	COW.				
ORGANISM	Bos taurus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.				
REFERENCE	1 (bases 1 to 489)				
AUTHORS	Smith, T.P.L., Grasse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.S., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-McKown, C.G., Perteau, G., Holt, I.I., Karanymcheva, S., Liang, F., Quackenbush, J. and Keel, J.W.				

BASE COUNT	112 a	140 c	160 g	77 t	
ORIGIN					
Query Match	33.1%	Score 383.2;	DB 11;	Length 489;	
Best Local Similarity	87.8%;	Pred. No. 6.6e-76;			
Matches 418;	Conservative	0;	Mismatches 58;	Indels 0;	Gaps 0;
QY	557	gateggtggactgcacagcccatgcttggcctgccgcggggggccaatttagagtgggtg	616		
Db	1	GACCGGTGGACTGCAGCAGCCATCACTGGGCCCTGTCGTGGGGGCCACTTGGAGGTGGTG	60		
QY	617	aacctctgc aaagccc atggagcgacaccaa atgtgagg gataa gctgctg agcacccccg	676		
Db	61	AGACTCTGCAGACCCGAGGAGCAGACACCAATGTGAGGGATAAGCTGCTGAGCACCCCC	120		
QY	677	ctgcacgtggcagtc ccggacagggc aggtggag attgtggagca ctttctatccctgggc	736		
Db	121	CTGCATCTGGCAGTCCCGAGCGGGCAGGTGGAGATCGTGGAACAATTTTCTATCCCTGGGC	180		
QY	737	ctgaatatcaatgccagacagggaaagg gatactccctgc atgatcgctgttaagctc	796		
Db	181	CTGACATCAATGCCAAGACAGAGAAGGGACAGCGCCCTGCATATGCTGTGAGGCTC	240		
QY	797	aaccgctaca aaatcat caaac tgc tgc tgc tgc atggggc tgc atgatg accaaga ac	856		

Db	241	AATCGCTACAAAATCATCAAAATGCTGCTCTGTCATGCGGCTGCATGATGAGCAGAAAC	300
Qy	857	ctggcaggaagaagaccgccagcgacctggtgcaagtctgtgcagtgctgatacccgccagcc	916
Db	301	CTGGCAGGAAGACCCCCACAGACCTTGGTGCAGCTGTGCGAAGCCGACACCCGGCAGCGT	360
Qy	917	ctggagcaatcctgagcgggggctgagcataacgggctggaggggcctaagtatgattggg	976
Db	361	CTGAGAACCTTCAGCCAGSGTTCAGAGCAGATGGACTGAGGGGTCCACCCGAGAGTGGG	420
Qy	977	cgagagacccctcagctgtgcagcccgatgaatgctgccccagcccgccagc	1032
Db	421	CGGGAGACCCCCAGCGCTGTGGCAGCCGAGTAATGCTGTCCGCGCTTACCAGG	476

Search completed: April 17, 2002, 09:26:13
Job time: 4617 sec

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